



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 165365

TO: **Phuong Bui**

Location: **rem/**

Art Unit: **1638**

Sept 14, 2005

Case Serial Number: 10/734698

From: **P. Sheppard**

Location: **Remsen Building**

Phone: **(571) 272-2529**

sheppard@uspto.gov

Search Notes

Interference

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 12, 2005, 21:01:33 ; Search time 835 Seconds
(without alignments)
3083.064 Million cell updates/sec

Title: US-10-734-698A-39

Perfect score: 2083

Sequence: 1 MATFTLFTSBSVNEGHPDKL.....GREDDPFTWVVKPLKWEKA 392

Scoring table:

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Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cgn2_1/USPTO.spool/US10734698/runat_12092005_134909_27452/app.query.fasta_1.583

-DB=Published Applications NA -QFMT=fastcap -SURF=rnpbp -MINMATCH=0.1

-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62

-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=ext -THR MAX=100

-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=exp -HEAPSIZ=500 -MINLEN=0

-MAXLEN=200000000 -USER=US10734698.cgn 1 1 800 @runat_12092005_134909_27452

-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100

-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5

-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2083	100.0	1465	18	US-10-425-114-10164 Sequence 10164, A
2	2083	100.0	1485	20	US-10-734-698A-38 Sequence 38, Appl
3	2083	100.0	1485	21	US-10-917-602A-38 Sequence 38, Appl
4	2083	100.0	1496	18	US-10-425-114-11983 Sequence 11983, A
5	2083	100.0	1518	17	US-10-431-252-1 Sequence 1, Appl
6	2083	100.0	1855	18	US-10-424-599-77204 Sequence 77204, A
7	2074	99.6	1509	18	US-10-425-114-29554 Sequence 29554, A
8	2073	99.5	1342	18	US-10-425-114-8517 Sequence 8517, Ap
9	2073	99.5	1349	18	US-10-425-114-11199 Sequence 11199, Ap
10	2073	99.5	1349	18	US-10-425-114-11868 Sequence 11868, A
11	2073	99.5	1427	18	US-10-425-114-12787 Sequence 12787, A
12	2073	99.5	1456	18	US-10-425-114-8399 Sequence 8399, Ap
13	2073	99.5	1456	18	US-10-425-114-10701 Sequence 10701, A
14	2073	99.5	1458	18	US-10-425-114-8336 Sequence 8336, Ap
15	2073	99.5	1461	18	US-10-425-114-8325 Sequence 8325, Ap
16	2073	99.5	1461	18	US-10-425-114-8325 Sequence 8325, Ap
17	2073	99.5	1468	18	US-10-425-114-11194 Sequence 11194, A
18	2073	99.5	1488	18	US-10-425-114-10273 Sequence 10273, A
19	2073	99.5	1488	18	US-10-425-114-7202 Sequence 7202, Ap
20	2073	99.5	1494	18	US-10-425-114-7368 Sequence 7368, Ap
21	2073	99.5	1494	18	US-10-425-114-10112 Sequence 10112, A
22	2073	99.5	1495	18	US-10-425-114-10262 Sequence 10262, A
23	2073	99.5	1505	18	US-10-425-114-11712 Sequence 11712, A
24	2073	99.5	1510	18	US-10-425-114-11050 Sequence 11050, A
25	2073	99.5	1514	18	US-10-425-114-8323 Sequence 8323, A
26	2073	99.5	1514	18	US-10-425-114-9591 Sequence 9591, Ap
27	2073	99.5	1514	18	US-10-425-114-10155 Sequence 10155, A
28	2073	99.5	1514	18	US-10-425-114-10248 Sequence 10248, A
29	2073	99.5	1515	18	US-10-425-114-8286 Sequence 8286, Ap
30	2073	99.5	1515	18	US-10-425-114-8286 Sequence 8286, Ap
31	2073	99.5	1515	18	US-10-425-114-9070 Sequence 9070, Ap
32	2073	99.5	1515	18	US-10-425-114-9087 Sequence 9087, Ap
33	2073	99.5	1515	18	US-10-425-114-9138 Sequence 9138, Ap
34	2073	99.5	1515	18	US-10-425-114-10041 Sequence 10041, A
35	2073	99.5	1515	18	US-10-425-114-11285 Sequence 11285, A
36	2073	99.5	1515	18	US-10-425-114-12737 Sequence 12737, A
37	2073	99.5	1523	18	US-10-425-114-12745 Sequence 12745, A
38	2073	99.5	1523	18	US-10-425-114-10819 Sequence 10819, A
39	2073	99.5	1529	18	US-10-425-114-10266 Sequence 10266, A
40	2060	98.9	1535	18	US-10-425-114-12664 Sequence 12664, A
41	2054	98.6	1538	18	US-10-424-599-77205 Sequence 77205, A
42	2046	98.2	1436	18	US-10-424-599-115395 Sequence 115395, A
43	2040.5	98.0	1459	18	US-10-424-599-77201 Sequence 77201, A
44	1999	96.0	1470	18	US-10-425-114-9680 Sequence 9680, Ap
45	1999	96.0	1479	18	US-10-425-114-13126 Sequence 13126, A
					US-10-425-114-11151 Sequence 11151, A

ALIGNMENTS

RESULT 1

US-10-425-114-10164

; Sequence 10164, Application US/10425114

; Publication No. US2004003488A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

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; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10164
; LENGTH: 1465
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700896469_FLI
US-10-425-114-10164

Alignment Scores:
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Score:          2083.00        Matches:      392
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              18           Gaps:       0

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DB 54 ATGGCAGAGACATTCTATTACCTCAGAGTCAGTGAGGAGGACACCTCGACAGCTC 113
QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerTys 40
DB 114 TGGCAGCAAAATCTCCGATGCTGCTCGAGCGTTCCTTGAACAGGACCCAGACGCAAG 173
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
DB 174 GTTGCCTGCGAAACATGSCACCAAGACCAACTTGGTCATGGTCTTCGGAGAGATCACACC 233
QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
DB 234 AAGGCCAACGTTGACTACGAGAGAGATCGTCGTGACCACTTCGAGGAACATCGGCTTCGTC 293
QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100
DB 294 TCAACAGATGTGGACTTCTGATGCTGACAACTGCAAGTCTCTTGTAAACATTGAGCAGCAG 353
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluIleGly 120
DB 354 AGCCCTTGATATTGCCAGAGGTGTGACGCGCCACCTTACCAGAAAGACCCGAGGAAATCGGT 413
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
DB 414 GCTGGAGACACAGGTCACATGTTTGGCTATGCCACGAGCAGACCCCAAGATTGATGCCA 473
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
DB 474 TTGAGTCATGTTCTTGCAACTAAACTCGGTGCTCGTCTCACCGAGGTTCCCAAGAACGGA 533
QY 161 ThrCysProThrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
DB 534 ACTTGCCCATGTTGAGGCTGTGATGGGAAGACCCCAAGTCACTGTTGAGTATTACAAATGAC 593
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
DB 594 AACGGTGCCATGGTTCCAGTTCGTGTCACACTGTGCTTATCTCCACCCCAATCATGTAG 653
QY 201 ThrValThrAsnAspGluIleAlaAspLeuLysGluHisValIleLysProValIle 220
DB 654 ACTGTGACCAACGACGAAATTGAGCTGACCTCAAGGAGCATGTGATCAAGCCGGTGATC 713
QY 221 ProGluLysThrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
DB 714 CCGGAGAAGTACTCTGATGAGAGACCAATTTCCACTTGAACCCCTCTGCGCGTTTTGTC 773
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
DB 774 ATTGGAGGTCTCTCACGGTGATGCTGCTCACCGGCGCAAGATCATCATCATCTTAC 833
QY 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
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DB 834 GGAGGATGGGCTGCTCATGTGGTGGTGCCTTCTCCGGGAAGGATCCCAAGAGTTGAT 893
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QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
DB 954 AGAGGTGCATTTGTGCAAGTGTCTTATGCCATTGGTGTGCCGAGCCCTTTGCTGCTCTT 1013
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
DB 1014 GTTGACACTTATGGCACCAGGATCCATGATAGGAGATTCTCAACATTGTGAAGGAG 1073
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyValAsn 360
DB 1074 AACTTTGATTTTCAGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAAT 1133
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
DB 1134 AACAGGTTCTTGAGAGACTGCTGCATATGCACACTTCGGCAGAGAGACCTTGACTTACA 1193
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
DB 1194 TGGGAAGTGGTCAAGCCCTCAAGTGGGAGAAGGCC 1229

RESULT 2
US-10-734-698A-38
; Sequence 38, Application US/10734698A
; Publication No. US20040209341A1
; GENERAL INFORMATION:
; APPLICANT: FALCO, SAVERIO CARL
; ALLEN, STEPHEN M.
; RAFALSKI, J. ANTONI
; HITZ, WILLIAM D.
; KINNEY, ANTHONY J.
; ABELL, LYNNE N.
; THORPE, CATHERINE J.
; TITLE OF INVENTION: PLANT AMINO ACID BIOSYNTHETIC ENZYMES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/734,698A
; FILING DATE: 12-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,771
; FILING DATE: 6-Jun-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MAJARIAN, WILLIAM R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1485 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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Db	974	AGAAGGTGCATTGTGCAAGTGTCTTATGTCATTGGTGTGCCGAGCCTTTGTCTGCTTT	1033
Qy	321	ValAspThrTyrGlyThrGlyIlysIleHisAspIysGluIleLeuAenIleValIysGlu	340
Db	1034	GTTTGACACCTTATGGCACCCGGGAAGATCCATGATTAAGGAGATTCTCAACATTGTGAAGGAG	1093
Qy	341	AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuIysArgGlyGlyAsn	360
Db	1094	AACCTTGATTTCAGGCCCGGTATGATCTCATCACTTGATCTCAAGAGGGGTGGGAAT	1153
Qy	361	AsnArgPheLeuIysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr	380
Db	1154	AACAGGTTCTTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGGACCCTGACTTCACA	1213
Qy	381	TTPGluValValIysProLeuIysTyrGluIysAla	392
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RESULT 3			
; Sequence 38, Application US/10917602A			
; Publication No. US20050120405A1			
; GENERAL INFORMATION:			
; APPLICANT: Falco, Saverio Carl			
; APPLICANT: Liu, Zhan-Bin			
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes			
; FILE REFERENCE: BB-1087 US CIP			
; CURRENT APPLICATION NUMBER: US/10/917,602A			
; CURRENT FILING DATE: 2004-08-13			
; PRIOR APPLICATION NUMBER: US 10/734698			
; PRIOR FILING DATE: 2003-12-12			
; PRIOR APPLICATION NUMBER: US 09/424978			
; PRIOR FILING DATE: 1999-12-02			
; PRIOR APPLICATION NUMBER: PCT/US98/11692			
; PRIOR FILING DATE: 1998-06-05			
; PRIOR APPLICATION NUMBER: 60/049,443			
; PRIOR FILING DATE: 1997-06-12			
; PRIOR APPLICATION NUMBER: US 60/048,771			
; PRIOR FILING DATE: 1997-06-06			
; NUMBER OF SEQ ID NOS: 69			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 38			
; LENGTH: 1485			
; TYPE: DNA			
; ORGANISM: Glycine max			
US-10-917-602A-38			
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Score:	2083.00	Matches:	392
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0
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Qy	21	CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys	40
Db	134	TGGGACAAATCTCCGATGCTGTCCTCGACGCTTGCTTGAACGAGGACCACAGCAGCAAG	193
Qy	41	ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr	60
Db	194	GTTGCTTGGCAACATGTCACCAAGACCACTTGCTCATGTGCTTTCGAGAGATCAACACC	253

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QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
DB 254 AAGGCCAAGCTTGACTACGAGAGAGATCGTGGTGACACCTCGCAGAACATCGGCTTCGTC 313
QY 81 SerAsnAspValGlyLeuAspAlaAspAenCysLysValLeuValAsnIleGluGln 100
DB 314 TCAACAGATGTGGACTTCATGCTGACAACTGCAAGTCTCTTGTAACATTCAGCAGCAG 373
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluIleGly 120
DB 374 AGCCCTGATATTGCCAGAGGTGTGACGGCCACCTTACAAAAGACCCGAGGAATCGGT 433
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
DB 434 GTTGGAGACAGGTCACATGTTTGGCTATGACGAGCAAAACCCAGAAATTGATGCCA 493
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
DB 494 TTGAGTCATGTTCTTGCAACTAAACTCGGTGCTCGTCTCACCGAGGTTCCGAAGAACGGA 553
QY 161 ThrCysProTrioLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
DB 554 ACCTGCCCATGTTGAGGCTGTATGGGAAAACCCCAAGTGACTGTTGAGTATTACAAATGAC 613
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
DB 614 AACGGTGCCATGGTTCAGTTGCTGTCACACTGTGCTTATCTCCACCACATGATGAG 673
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
DB 674 ACTGTGACCAACGACGAAATTGACGTGACCTCAAGAGCATGTGATCAAGCGGTGATC 733
QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
DB 734 CCGGAGAACTACTTGATGAGAAGACCAATTTCCACTTGAAACCCCTCTGGCCGTTTGTG 793
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
DB 794 ATTGGAGTCTCTACGGTGATGCTGCTCTCACCGGCCGCAAGATCATCATCTACTTAC 853
QY 261 GlyGlyTrioGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
DB 854 GGAGGATGGGTGCTCATGCTGCTGCTGCTCTCCGGGAAGGATCCCAACCAAGGTTGAT 913
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
DB 914 AGAGTGGGTTCATATTGTGACAGGCTGTCTAAGAGCATTTGTGCAAGTGGACTAGCC 973
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
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QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
DB 1034 GTTGACACCTATGGCACCGGGAAGATCCATGATAAGGAGATTCCTCAACATTTGTGAAGGAG 1093
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLysArgGlyGlyAsn 360
DB 1094 AACTTTGATTTTCAAGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAAT 1153
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
DB 1154 AACAGGTTCTTGAGACTGCTGCATATGGACACTTCGGCAGAGAGACCTTGACTTCACA 1213
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
DB 1214 TGGGAAGTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249
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RESULT 4

US-10-425-114-11983

; Sequence 11983, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

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; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack B
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 11983
; LENGTH: 1496
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701150545_FLI
US-10-425-114-11983
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Alignment Scores: 2.58e-228 Length: 1496
Pred. No.: 2083.00 Matches: 392
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 18
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US-10-734-698A-39 (1-392) x US-10-425-114-11983 (1-1496)

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QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
DB 86 ATGGCAGAGACATTCTTATTACCTCAGAGTCAGTGAACGAGGACACCTCGACAAGCTC 145
QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
DB 146 TGCACCAAAATCTCGATGCTGCTCGACGCTTGCCCTTGAACAGGACCCAGACAGCAAG 205
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
DB 206 GTTGCTCTCGAAACATGACACTTAAGACCAACTTGGTCATGGTCTTCGGAGAGATCACACC 265
QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
DB 266 AAGGCCAAGCTTGACTACGAGAGATCGTGGTGACACCTCGCAGGAACATCGGCTTCGTC 325
QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 100
DB 326 TCAACAGATGTGGGACTTGATGCTGACAACTGCAAGGTCTTGTAAACATTTGAGCAGCAG 385
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
DB 386 AGCCCTGATATTGCCAGGCTGTGACGGCCACCTTACAAAAGACCCGAGGAATTCGCT 445
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
DB 446 GCTCGAGACCAAGGTCACATGTTTGGCTATGCCAGGACGAGACCCAGAAATTGATGCCA 505
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
DB 506 TTGAGTCATGTTCTTGCAACTTAAACTCGGTGCTCGTCTCACCGAGGTTTCGAAGAACGGA 565
QY 161 ThrCysProTrioLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
DB 566 ACCTGCCCATGTTGAGGCTGTATGGGAAAGACCCAGTACTGTTGAGTATTACAAATGAC 625
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
DB 626 AACGGTGCCATGGTTCAGTTGCTGTCACACTGTGCTTATCTCCACCACATGATGAG 685
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
DB 686 ACTGTGACCAACGAGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCCGCTGATC 745
```


QY 381 TrrGluValValysProLeuLysTrrGluLysAla 392
 DB 1214 TGGGAAGTGGTCAAGCCCTCAAGTGGGAGAGGCC 1249

RESULT 6

US-10-424-599-77204
 ; Sequence 77204, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 77204
 ; LENGTH: 1855
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_40730C.1
 US-10-424-599-77204

Alignment Scores:
 Pred. No.: 3,5e-228 Length: 1855
 Score: 2083.00 Matches: 392
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-424-599-77204 (1-1855)

QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
 DB 140 ATGGCAGAGACATTTCTATTACCTCAGAGTCAGTGAACGAGGGACACCTCAGCAAGCTC 199
 QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
 DB 200 TGGGACCAAAATCTCCGATGCTCTCGAGCTTGCTTGAACAGGACCCAGACAGCAAG 259
 QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
 DB 260 GTTGCCTGGAAACATGCACCAAGACCAACTTTGGTTCATGGTCTTCGAGAGATCACCACC 319
 QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
 DB 320 AAGGCCAACCGTTGACTACGAGAAGATCGTGCCTGACACCTGCAGGAAACATCGCTTCGTC 379
 QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100
 DB 380 TCAACGATGTGGAGCTTGAATGCTGCACTGCAAGTCTCTGTAAACATTGAGCAGCAG 439
 QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
 DB 440 AGCCCTGATATTGCCCGAGGTGTGACGCGCCACCTTACCAGGAGCCCGAGGAAATCGGT 499
 QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
 DB 500 GTGGAGACCGAGGTTCACATGTTGGCTATGCCACGAGCAGACCCCAAGTTGATGCCA 559
 QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
 DB 560 TTGAGTATGTTCTTCAACTAACTCCGTGCTCGTCTCACCAGGTTCCGAGAACCGGA 619
 QY 161 ThrCysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTrpAsnAsp 180
 DB 620 ACCTGCCCATGGTTGAGGCTGTATGGGAGAGCCCAAGTGACTGTTGAGTATTACAATGAC 679

QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuLysSerThrGlnHisAspGlu 200
 DB 680 AACGGTGCATGGTTCAGTTCGCTGTCACACTGCTTATCTCCACCAACATGATGAG 739
 QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
 DB 740 ACTGTGACCAACGACGAAATTCAGCTGACCTCAAGGAGCATGTGATCAAGCGGTGATC 799
 QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
 DB 800 CCGGAGAAAGTACCTTGTGAGAGAACCACTTTTCCACTTGAACCCCTCTGGCGTTTGTGTC 859
 QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyr 260
 DB 860 ATTGGAGTCTCTCAGGAGTGTGCTGTCTCAGCGGCCGCAAGATCATCATGATACTTAC 919
 QY 261 GlyGlyTrrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
 DB 920 GGAGGATGGGTGCTCATGTTGGTGGTCTCTCCGGGAAGGATCCCAAGGTTGAT 979
 QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAla 300
 DB 980 AGGAGTGGTGTCTTCAATTGTGAGACAGGCTGCTAAGAGCATTTGTGSCAAGTGGACTAGCC 1039
 QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
 DB 1040 AGAAGTGCATTGTGCAAGTGTCTTATGCCATTGGTGTGCGGAGCCCTTGTCTGTCTTT 1099
 QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
 DB 1100 GTTGACACCTATGGCAGCGGAAGATCCATGATAGGAGATTTCTCAACATTGTGAAGGAG 1159
 QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyClyAsn 360
 DB 1160 AACTTTGATTTTCAGGCCCGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGGAAT 1219
 QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
 DB 1220 AACAGGTTCTTGAAGACTGCTGCATATGACACTTCCGACAGAGAGACCTTGACTTTCACA 1279
 QY 381 TrpGluValValysProLeuLysTrpGluLysAla 392
 DB 1280 TGGGAAGTGGTCAAGCCCTCAAGTGGGAGAGGCC 1315
 RESULT 7
 US-10-425-114-29554
 ; Sequence 29554, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 29554
 ; LENGTH: 1509
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: UC-GMFLMINSOY064D01_FLI
 US-10-425-114-29554

Alignment Scores:
 Pred. No.: 2,82e-227 Length: 1509
 Score: 2074.00 Matches: 390

Percent Similarity:	99.74%	Conservative:	1
Best Local Similarity:	99.49%	Mismatches:	1
Query Match:	99.57%	Indels:	0
DB:	18	Gaps:	0
US-10-734-698A-39 (1-392) x US-10-425-114-29554 (1-1509)			
Qy	1	MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu	20
Db	89	ATGGCAGAGACATTCTCTATTACCTCAGAGTCGGTGAACGAGGACACCCCTGACAGCTC	148
Qy	21	CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys	40
Db	149	TGGCAGCAAAATCTCCGATGCTGCTCGACGCTTGGCTCGAGCAGGACCCAGACAGCAAA	208
Qy	41	ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr	60
Db	209	GTTGCTCGCAAAACATGCACCAAAACCACTTGGTCATGTCTTCGGAGAAATCAGACC	268
Qy	61	LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal	80
Db	269	AAGGCCAACCTTGACTACGAGAAGATAGTCGTGACACCTGCAGGAACATCGGCTTCGTC	328
Qy	81	SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln	100
Db	329	TCAAATGATGTGGACTGGATGCCACAACTGCAAGGTCTCTGTCACCATTTGAGCAGCAG	388
Qy	101	SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly	120
Db	389	AGCCCTGATATTGCTCAGGGGTATACCGGCACCTTACCAAAACCTCGAAGAAATGGT	448
Qy	121	AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro	140
Db	449	GCTGGTGACCGGTACATGTTTGGCTATGCCACTGATGAAACCCCTGATTTGATGCCA	508
Qy	141	LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly	160
Db	509	TTGAGCCATGTTCTTGCAACAAACTCGGTGCTCGTCTCACCGAGGTTTCGCAAGACGGT	568
Qy	161	ThrCysProThrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp	180
Db	569	ACCTGCCCTTGGCTGAGGCTGTATGGGAAGACCAAGTGAACCTTGAGTATTAATGAC	628
Qy	181	AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu	200
Db	629	AATGGTGCCAGGTTCCGGTTGGTGTCCACACCGTGTCTAATCTCCACCAACACGACGAG	688
Qy	201	ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle	220
Db	689	ACTGTCAACCAATGACGAAATGTGCTGACCTCAAAGAGCATGTGATCAAGCCTGTGATC	748
Qy	221	ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal	240
Db	749	CCAGAGAAGTACCTTGATGAGAAGACCATTTTCCACTTGAAACCTTCAGCCCGTTTGTG	808
Qy	241	IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyr	260
Db	809	ATTGGTGGCCCTCATGSCGATGCTGGTCTCACCGCGCGCAAGATCATTCGATACTTAT	868
Qy	261	GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp	280
Db	869	GGAGGATGGGTGCTCATGTGTGTGGTGTCTTCTCCGGGAAGACCCCTACCAAGGTTGAT	928
Qy	281	ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLysLeuAla	300
Db	929	AGAGTGGTCTTACATTGTGACAGAGCTGCTTAAGAGCATTTGTGCAAGTGGACTTGCC	988
Qy	301	ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe	320
Db	989	AGAAGGTGCATTGTGCAAGTGTCTATGCCATTGGTGTGCTCGAGCCTTTGCTGTGTTT	1048
Qy	321	ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu	340

Db	1049	GTTGACACCTATGGCACTGGGAAGATCCATGATTAAGAGATTTCTCAACATTTGTAAGGAA	1108
Qy	341	AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn	360
Db	1109	AACTTTGATTTTCAGGCTGGTATGATCTCCATCAACTTGATCTCAAGAGGGTGGAAAT	1168
Qy	361	AsnArgPheLeuLysThrAlaIaTyrGlyHisPheGlyArgGluAspProAspPheThr	380
Db	1169	AACAGGTTTTTGAAGACTGCTGCTATGGACACTTTTGAAGAGAGAGACCCCTGATCTTCA	1228
Qy	381	TrpGluValValLysProLeuLysTrpGluLysAla	392
Db	1229	TGGGAAGTGGTCAAAACCCCTCAAGTGGGAGAGGCC	1264
RESULT 8			
US-10-425-114-8517			
; Sequence 8517, Application US/10425114			
; Publication No. US20040034888A1			
; GENERAL INFORMATION:			
; APPLICANT: Liu, Jingdong			
; APPLICANT: Zhou, Yihua			
; APPLICANT: Kovalic, David K.			
; APPLICANT: Screen, Steven E.			
; APPLICANT: Tabaska, Jack E.			
; APPLICANT: Cao, Yongwei			
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With			
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement			
; FILE REFERENCE: 38-21(5313)B			
; CURRENT APPLICATION NUMBER: US/10/425,114			
; CURRENT FILING DATE: 2003-04-28			
; NUMBER OF SEQ ID NOS: 73128			
; SEQ ID NO 8517			
; LENGTH: 1342			
; TYPE: DNA			
; ORGANISM: Glycine max			
; FEATURE:			
; OTHER INFORMATION: Clone ID: 700757167_FLI			
US-10-425-114-8517			
Alignment Scores:			
Pred. No.:	3,11e-227	Length:	1342
Score:	2073.00	Matches:	389
Percent Similarity:	99.74%	Conservative:	2
Best Local Similarity:	99.23%	Mismatches:	1
Query Match:	99.52%	Indels:	0
DB:	18	Gaps:	0
US-10-734-698A-39 (1-392) x US-10-425-114-8517 (1-1342)			
Qy	1	MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu	20
Db	95	ATGGCAGAGACATTCTCTATTACCTCAGAGTCGGTGAACGAGGACACCTGCAAGCTC	154
Qy	21	CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys	40
Db	155	TGCAGCAAAATCTCCGATGCTGCTCGACGCTTGCCTCGACGAGACCCAGACAGCAA	214
Qy	41	ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr	60
Db	215	GTTGCTCGCAAAACATGCACCAAAACCAACTTGGTCTATGCTCTTCGGAGAAATCAGACC	274
Qy	61	LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal	80
Db	275	AAGGCCAACCTTGACTACGAGAAGATAGTGGCTGACACCTCGCAGGAACATCGGCTTCGTC	334
Qy	81	SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln	100
Db	335	TCAAATGATGTGGGACTGGATGCCACAACTCCAAAGGTCTCTGTCACCATTTGAGCAGAG	394
Qy	101	SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly	120
Db	395	AGCCCTGATATTGCTCAGGGTGTACACGCCACCTTACCAAAAAACCTCGAAGAAATGGT	454

121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
161 ThrCysProTyrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
181 AsnGlyAlaMetValProValArgValHisThrValLeuLeuSerThrGlnHisAspGlu 200
201 ThrValThrAsnAspGluLeuAlaAlaAspLeuLysGluHisValLysProValIle 220
221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyLysAsn 360
361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
381 TrpGluValValLysProLeuLysTrpGluLysAla 392
1235 TGGGAAGTGGTCAAAACCCCTCAAGTGGGAGAGGCC 1270

RESULT 9

US-10-425-114-11199
; Sequence 11199, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(S3313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 11199
; LENGTH: 1349
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701040251_FLI
US-10-425-114-11199

Alignment Scores:
Pred. No.: 3.13e-227 Length: 1349
Score: 2073.00 Matches: 389
Percent Similarity: 99.74% Conservative: 2
Best Local Similarity: 99.23% Mismatches: 1
Query Match: 99.52% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-425-114-11199 (1-1349)

Qy 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
Db 85 ATGGCAGACACATTCTTATTTACCTCAGAGTCGGTGAACGAGGACACCTGACAGCTC 144
Qy 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
Db 145 TGCACCAAAATCTCCGATGCTGCTCGACGCTTGGCTCGAGCAGGCCACGACAGCAAA 204
Qy 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
Db 205 GTTGCTCGCAAAACATGCACAAACCAACTTGGTTCATGGTCTTCGAGAAATCATCGACC 264
Qy 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
Db 265 AAGGCCAACGTTGACTACGAGAGATAGTGGTGACACTCGAGGAAACATCGGCTTCGTC 324
Qy 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 100
Db 325 TCAAAATGATGTGGGACTGGATGCCGACAACTGCAAGGTCTCGTCAACATTGAGCAGCAG 384
Qy 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
Db 385 AGCCCTTGATATTTGCTCAGGGGTGTACACGCCACCTTACCAAAAAACCTGAAAGAAATTGGT 444
Qy 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
Db 445 GCTGGTGACAGGGTCACATGTTGGCTATGCCACTGATGAAACCCCTGAAATTGATGCCA 504
Qy 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
Db 505 TTGAGCCCATGTTCTTGCACAAAACTCGGTGCTGCTCTCACCGAGGTTTCGCAAGAACGGT 564
Qy 161 ThrCysProTyrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
Db 565 ACCTGCCCCCTGGCTGAGGCCCTGATGGGAAAGACCCCAAGTGACCGTTGAGTATTACAAATGAC 624
Qy 181 AsnGlyAlaMetValProValArgValHisThrValLeuLysSerThrGlnHisAspGlu 200
Db 625 AATGGTGCCAGGGTTCCTATTCTGTGTACACACCGCTGCTAATCTCCACCCACACGACGAG 684
Qy 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValLysProValIle 220
Db 685 ACTGTACCAATGACGAAATTTGCTGCTGACCTCAAGAGCATGTGATCAAGCCTGTGATC 744
Qy 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
Db 745 CCAGAGAAAGTACCTTGATGAGAAAGCAATTTTCCACTTGAACCCCTTCAGGCCGTTTGTGTC 804
Qy 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
Db 805 ATTGGTGGCCCTCATGGCGATGCTGGTCTCACCGGCCCGCAGATCATTTATCGATCTTAT 864
Qy 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
Db 865 GGAGGATGGGTGCTCATGGTGGTGGTCTTTCTCCGGGAAGGACCTTACCAAGGTTGAT 924

QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
DB 925 AGGAGTGGTCTTACATTGTGAGACAGGCTGCTAAGAGCATTGTGGCAAGTGGACTTGCC 984
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
DB 985 AGAAGGTGCATTGGCAAGTGTCTTATGCCATTGGTGTGCTGAGCCCTTTGTCTGTGTTT 1044
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
DB 1045 GTTGACACCTATGGCATCGGAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAA 1104
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
DB 1105 AACTTTGATTTCAGGCTGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGAAT 1164
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
DB 1165 AACAGGTTTTTGAAGACTGTGCTCTATGACACTTTTGAAGAGAGAACCCCTGACTTCACA 1224
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
DB 1225 TGGGAAGTGTCTCAACCCCTCAAGTGGGAGAGGCC 1260

RESULT 10
US-10-425-114-11868
; Sequence 11868, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 11868
; LENGTH: 1349
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701137731_FLI
US-10-425-114-11868

Alignment Scores:
Pred. No.: 3,13e-227 Length: 1349
Score: 2073.00 Matches: 389
Percent Similarity: 99.74% Conservative: 2
Best Local Similarity: 99.23% Mismatches: 1
Query Match: 99.52% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-425-114-11868 (1-1349)

QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
DB 89 ATGGCAGAGACATTCTTATTTACCTCAGAGTCGGTGAACGAGGAGACACCCCTGACAAAGCTC 148
QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
DB 149 TGGACACCAATCTCCGATGTGCTCTGACGCTTGCCCTCGAGCAGGACCCAGACAGCAAA 208
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
DB 209 GTTGCCTCGCAACATGCACCAAAACCACTTGGTCATGTCTCTCGGAGAAATCAGACC 268
QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80

DB 269 AAGGCCAACGTTGACTACGAGAAGATAGTGCCTGACACCTGCAGGAACATCGCTTCGTC 328
QY 81 SerAsnAspValGlyLeuAspAlaAspAenCysValLeuValLeuValAsnIleGluGlnGln 100
DB 329 TCNAATGATGTGGACTGGATGCCGACAACTGCAGGTCCTGCTCAACATTGAGCAGCAG 398
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
DB 389 AGCCCTGATATTGCTCAGGCTGTACAGGCCACCTTACCAAAAAACCTGAAGAAATGGT 448
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
DB 449 GCTGSGTACACCGGTCACATGTTGGCTATGCCACTGATGAACCCCTCAATTGATGCCA 508
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
DB 509 TTGAGCCATGTTCTTGCACAAACCTCGGTGCTGCTCACCAGGTTCCGCAAGACGGT 568
QY 161 ThrCysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
DB 569 ACTGCGCCTTGGCTGAGGCTGATGGGAAGACCCAAAGTGACCGTTGAGTATTACAATGAC 628
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
DB 629 AATGSGTCCAGGTTCTTATTCGTGTACACACCGTCTAATCTCCACCCCAACACGACGAG 698
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
DB 689 ACTGTCAACCATGACGAAATTCGTCTGACTCTCAAGAGCATGTGATCAAGCCTGTGATC 748
QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
DB 749 CCAGAGAAGTACCTTGATGAGAAGACCAATTTCCACTTGAACCCCTTCAGGCCGTTTGTG 808
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyr 260
DB 809 ATTGSGGCCCTCATGGCGATGCTGCTCACCGGCCGCAAGATCATTAATCATGACTTAT 868
QY 261 GlyGlyTyrGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
DB 869 GGAGAGATGGGTGCTCATGCTGTGTGCTTTCTCCGGGAAGGACCCCTACCAAGTTGAT 928
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAla 300
DB 929 AGGAGTGGTGTTCATCTGTGAGACAGGCTGCTAAGAGCATTGTGGCAAGTGGACTTGC 988
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
DB 989 AGAAGGTGCATTGTGCAAGTGTCTTATGCCATTGGTGTGCTGAGCCCTTTGTCTGTGTTT 1048
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
DB 1049 GTTGACACCTATGGCACTGGGAAGATCCATGATAGGAGATTCTCAACATTGTGAAGGAA 1108
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
DB 1109 AACTTTGATTTTCAGGCTGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGAAT 1168
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
DB 1169 AACAGGTTTTTGAAGACTGTGCTCTATGACACTTTTGAAGAGAGAACCCCTGACTTCACA 1228
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
DB 1229 TGGGAAGTGTCTCAACCCCTCAAGTGGGAGAGGCC 1264

RESULT 11

US-10-425-114-12787
; Sequence 12787, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong

```
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 12787
; LENGTH: 1427
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701211701_FLI
US-10-425-114-12787

Alignment Scores:
Pred. No.: 3,39e-227 Length: 1427
Score: 2073.00 Matches: 389
Percent Similarity: 99.74% Conservative: 2
Best Local Similarity: 99.23% Mismatches: 1
Query Match: 99.52% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-425-114-12787 (1-1427)

QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
DB 65 ATGGCAGAGACATTCTATTACCTCAGAGTCGGTGAACAGGAGCACCCCTGACAAGCTC 124
QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
DB 125 TGGCAGCAAAATCTCCGATGCTGCTCGACGCTTGCCTCGAGCAGGACCACAGACGCAA 184
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
DB 185 GTTGCTCGGAACATCGACCAAAACCACTTGGTCATGGTCTTCGGAGAAATCAGACC 244
QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
DB 245 AAGGCCAACGTTGACTACGAGAAGATAGTGGTGACACCTGCAGGAACAATCGGCTTCGTC 304
QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100
DB 305 TCAAAATGATGTGGGACTGGATGCCGCAACTGCAAGGTCTCGTCAACATTGAGCAGCAG 364
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
DB 365 AGCCCTGATATTGCTCAGGGTGTCACGGCCACCTTACCAAAAACCTGAGAAATTTGT 424
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
DB 425 GCTGGTGACCGGTCACATGTTTGGCTATGCCACTGATGAACCCCTGAATTGATGCCA 484
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysIleGly 160
DB 485 TTGAGCCATGTTCTTGCACAAACAACTCGGTGCTCGTCTCACCAGGTTTCGCAAGAACGCT 544
QY 161 ThrCysProTyrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
DB 545 ACCTGCTGCTGGCTGAGGCTGATGGGAAGACCAAGTAGCCGTTGAGTATTACATGAC 604
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
DB 605 AATGGTGCCAGGGTTCCTATTCTGTGTACACACCGTCTAATCTCCACCCCAACACGACGAG 664
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
DB 665 ACTGTACCAATGACGAAATGCTGTGACCTCAAGAGCATGTGATCAAGCCTGTGATC 724
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QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
DB 725 CCAGAGAAGTAGCTTGATGAGAGACCAATTTTCCACTTGAACCCCTTCAGGCGGTTTTGTC 784
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
DB 785 ATTGGTGGCCCTCATGTGGCATGCTGTCTCACCGGCCGCAAGATCATTCGATACTTAT 844
QY 261 GlyGlyTyrGlyAlaHisGlyGlyValaPheSerGlyLysAspProThrLysValAsp 280
DB 845 GGAGGATGGGTGCTCATGGTGGTGGTCTTCTCCGGAAGGACCTTACCAAGGTTGAT 904
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
DB 905 AGGAGTGGTGTACATTGTCAGACAGGCTGCTAGAGCATTTGTGGCAAGTGGACTTGGCC 964
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
DB 965 AGAAGGTGCATTGTGCAAGTGTCTTATGCCATTGGTGGCTGAGCCCTTGTCTGTGTTT 1024
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
DB 1025 GTTGACACCTATGGCAGCTGGGAAGATCCATGATAAGGAGATTTCTCAACATTGTGAAGGAA 1084
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
DB 1085 AACTTTGATTTTCAGGCTGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGAAT 1144
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
DB 1145 AACAGGTTTTTGAAGACTGCTGCCCTATGGACACTTTTGAAGAGAGACCCCTGACTTCACA 1204
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
DB 1205 TGGGAAGTGGTCAAAACCCCTCAAGTGGGAGAAGGCC 1240

RESULT 12
US-10-425-114-8399
; Sequence 8399, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8399
; LENGTH: 1456
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700751645_FLI
US-10-425-114-8399

Alignment Scores:
Pred. No.: 3,49e-227 Length: 1456
Score: 2073.00 Matches: 389
Percent Similarity: 99.74% Conservative: 2
Best Local Similarity: 99.23% Mismatches: 1
Query Match: 99.52% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-425-114-8399 (1-1456)

QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
```

Db 90 ATGGCAGAGACATCTCTATTATTAACCTCAGATCGGTGAACGAGGGACACCCCTGCAAGCTC 149
Qy 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
Db 150 TGGCACCANAATCTCCGATGCTGTCTCGACGCTTGCTCGAGCAGGACCCAGACAGCAA 209
Qy 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
Db 210 GTTGCCTCGCAAAACATGCACCAAAACCACTTGCTGATGCTTTCGGAGAAATTCAGACC 269
Qy 61 LysAlaAsnValAspTyrGluLysIleValLysAspThrCysArgAsnIleGlyPheVal 80
Db 270 AAGCCCAACGTTGACTACGAGAGATAGTGGTGACACCTGCAGGAACATCGCGCTTCGTC 329
Qy 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 100
Db 330 TCAATGATGTGGACTGGATGCCCAACTGCAAGTCTCTCAACATTGAGCAGCAG 389
Qy 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
Db 390 AGCCCTGATATTGCTCAGGGGTACACGGCCACCTTACCACCAAAACCTGAAGAAATTTGGT 449
Qy 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
Db 450 GCTGGTGACGAGGTCACATGTTGGCTATGCCACATGATGAACCCCTGAATTGATGCCA 509
Qy 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
Db 510 TTGAGCCATGTTCTTGCAACAAACTCGGTGCTCGTCTCACCGAGGTTCCGAAGACGGT 569
Qy 161 ThrCysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
Db 570 ACCTGCGCTTGGCTGAGGCTGATGGAGAACCCAAAGTGACCTGATCAAGCTGTGATC 629
Qy 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
Db 630 AATGGTGGCCAGGGTTCCTATTCTGTGTACACACCGCTGAATCTCCACCCCAACACGACGAG 689
Qy 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
Db 690 ACTGTACCNAATGACGNAATGTGTGCTGACCTCAAGAGCATGTGATCAAGCTGTGATC 749
Qy 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
Db 750 CCAGAGAAGTACCTTGATGAGAAGACCATTTTCCACTTGAACCTTTCAGGCCGCTTTTGTG 809
Qy 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
Db 810 ATTGGTGGCCCTCATGGCGATGCTGGTCTCACCGCCGCAAGATCATTTATCGATACCTTAT 869
Qy 261 GlyGlyTyrGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
Db 870 GGAAGATGGGTGCTCATGGTGGTGGTGTCTTCTCCGGGAGACCCCTACCAGGTTGAT 929
Qy 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
Db 930 AGCAGTGGTCTTACATTGTGACAGAGCTGTCAAGAGCATTTGTGCAAGTGGACTTGGC 989
Qy 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
Db 990 AGAAGGTGCATTGTGCAAGTGTCTTATGCAATGGTGTGGCTGAGCCTTTGCTGTGTTT 1049
Qy 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
Db 1050 GTTGACACCTATGGCACTGGGAAGATCCATGATGAAGAGATTCTCAACATTGTGAAGGAA 1109
Qy 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
Db 1110 AACTTTGATTTCAGGCTGATATGATCTCCATCAACCTTATCTCAAGAGGGGTGGAAT 1169
Qy 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
Db 1170 AACAGGTTTTTGAAGACTGTCTGCTATGGACACTTTTGGAGAGAACCCCTGATCTTCA 1229

Qy 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
Db 1230 TGGGAAGTGGTCAAAACCCCTCAAGTGGGAGAAGGCC 1265

RESULT 13

US-10-425-114-10701
; Sequence 10701, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10701
; LENGTH: 1456
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700961178_FLI
US-10-425-114-10701

Alignment Scores:
Pred. No.: 3,49e-227 Length: 1456
Score: 2073.00 Matches: 389
Percent Similarity: 99.74% Conservative: 2
Best Local Similarity: 99.23% Mismatches: 1
Query Match: 99.52% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-425-114-10701 (1-1456)

Qy 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
Db 90 ATGGCAGAGACATCTCTATTATTAACCTCAGATCGGTGAACGAGGGACACCCCTGCAAGCTC 149
Qy 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
Db 150 TGGCACCANAATCTCCGATGCTGTCTCGACGCTTGCTCGAGCAGGACCCAGACAGCAA 209
Qy 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
Db 210 GTTGCCTCGCAAAACATGCACCAAAACCAACTTGGTCTGCTCGAGGACCCAGACAGCAA 269
Qy 61 LysAlaAsnValAspTyrGluLysIleValLysAspThrCysArgAsnIleGlyPheVal 80
Db 270 AAGCCCAACGTTGACTACGAGAGATAGTGGTGACACCTGCAGGAACATCGCGCTTCGTC 329
Qy 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 100
Db 330 TCAATGATGTGGACTGGATGCCCAACTGCAAGTCTCTCAACATTGAGCAGCAG 389
Qy 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
Db 390 AGCCCTGATATTGCTCAGGGGTACACGGCCACCTTACCACCAAAACCTGAAGAAATTTGGT 449
Qy 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
Db 450 GCTGGTGACGAGGTCACATGTTGGCTATGCCACATGATGAACCCCTGAATTGATGCCA 509
Qy 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
Db 510 TTGAGCCATGTTCTTGCAACAAACTCGGTGCTCGTCTCACCGAGGTTCCGAAGACGGT 569
Qy 161 ThrCysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180

Db 570 ACCTGCCCTTGGCTGAGGCTGATGGAGACCCCAAGTGCCTGGATTACAAATGAC 629
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
Db 630 AATGGTGCACGGGTTCTTATTCGTGTACACACCGCTGCTAATCTCCACCCCAACACGACGAG 689
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
Db 690 ACTGTCACCAATGACGAAATTCGTGCTGACCTCAAGAGCATGTGATCAAGCCTGTGATC 749
QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
Db 750 CCAGAGAAGTACCTTGTATGAGAAGACCAATTTCCACTTCAACCCCTCAGCCGCTTTGTC 809
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
Db 810 ATTGGTGGCCCTCATGCGCATGCTGTCTCACCGGCCGCAAGATCATTTATCGATACTTAT 869
QY 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
Db 870 GGAGGATGGGTGCTCATGTGTGTGTCTTCTCCGGGAAGACCCCTACCAAGGTTGAT 929
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
Db 930 AGGAGTGGTGTACATTGTGACACAGGCTGCTAAGAGCATTTGTGCAAGTGGACTTGC 989
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
Db 990 AGAAGGTGCATTGTGCNAGTGTCTTATGCCATTGGTGTGCTGAGCCTTTGTCTGTGTTT 1049
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
Db 1050 GTTGACACCTATGGCACTGGAGAGATCCATGATAGAGATTTCTCAACATTGTGAGGAA 1109
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
Db 1110 AACTTTGATTTCAGGCTCGTATGATCTCCATCAACCTTGTATCTCAAGAGGGGTGGAAT 1169
QY 361 AsnArgPheLeuLysThrAlaIleTyrGlyHisPheGlyArgGluAspProAspPheThr 380
Db 1170 AACAGGTTTTTGAAGACTGCTGCTATGACACTTTTGAAGAGAGAACCCCTGACTTCACA 1229
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
Db 1230 TGGGAAGTGGTCAACCCCTCAAGTGGAGAGGCC 1265

RESULT 14
US-10-425-114-8336
; Sequence 8336, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8336
; LENGTH: 1458
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700748001_FLI
US-10-425-114-8336
Alignment Scores:

Pred. No.: 3-5e-227 Length: 1458
Score: 2073.00 Matches: 389
Percent Similarity: 99.74% Conservatives: 2
Best Local Similarity: 99.23% Mismatches: 1
Query Match: 99.52% Indels: 0
DB: 18 Gaps: 0
US-10-734-698A-39 (1-392) x US-10-425-114-8336 (1-1458)
QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
Db 92 ATGGCAGAGACATTCTTATTTACCTTCAGATCGGTGTAACGAGGGACACCTCTGACAAGCTC 151
QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
Db 152 TCGGACCAAAATCTCGATGCTGTCTCGACGCTTGCCCTCGAGCAGACCCGACAGACAAA 211
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
Db 212 GTTGCTCGGAAACATGCACCAAAACCAACTTGGTCATGGTCTTCGGAGAAATCACGACC 271
QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
Db 272 AAGGCCAAACGTTGACTACGAGAAGATAGTGGCTGCACACTGCAGGAGACATCGGCTTCGTC 331
QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100
Db 332 TCAATGATGTGGGACTGGATGCCGACAACTGCAAGGTCTCGTCAACATTGAGCAGCAG 391
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
Db 392 AGCCCTGATATTGCTCAGGGGTGTACACGCCACACTTACCAAAAAACCTTGAAGAAATGGT 451
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
Db 452 GCTGTGTACACGGGTACATGTTTGGCTATGCCATGATGAACCCCTTGAATTTGATGCCA 511
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyValAlaArgLeuThrGluValArgLysAsnGly 160
Db 512 TTGACCAATGTTCTTGGCAACAAACTCGGTGCTGCTCTCACCGAGGTTCCGACAGAACCGT 571
QY 161 ThrCysProTyrLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
Db 572 ACCTGCCCTTGGCTGAGGCCCTGATGGGAAGACCCCAAGTGACCGTTGAGTATTACAATGAC 631
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
Db 632 AATGGTGCACGGGTTCTTATTCGTGTACACACCGGTGCTTAATCTCCACCCCAACACGACG 691
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
Db 692 ACTGTCACCAATGACGAAATTCGTGCTGACCTCAAGAGCATGTGATCAAGCCTGTGATC 751
QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
Db 752 CCAGAGAAGTACCTTGTATGAGAAGACCAATTTCCACTTGAACCCCTTCAAGCCGCTTTGTC 811
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
Db 812 ATTGGTGGCCCTCATGCGCATGCTGTCTCACCGGCCGCAAGATCATTTATCGATACTTAT 871
QY 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
Db 872 GGAGGATGGGTGCTCATGTTGGTGTGCTTCTCCGGGAAGGACCCCTACCAAGGTTGAT 931
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAla 300
Db 932 AGGAGTGGTGTACATTGTGAGACAGGCTGCTAAGAGCATTTGTGCAAGTGGACTTGC 991
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
Db 992 AGAAGGTGCATTGTGCAAGTGTCTTATGCCATTGGTGTGCTGAGCCCTTTGTCTGTGTTT 1051

QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
Db 1052 GTTGACACCTATGGCACTGGGAAGATCCATGATAAGAGATTCTCAACATTGTGAAGGAA 1111
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLysArgGlyGlyAsn 360
Db 1112 AACTTTGATTTCAGGCGTGGTATGATCTCCATCAACCTTGATCTCAAGAGGGGTGGAAT 1171
QY 361 AsnArgPheLeuLysThrAlaIleTyrGlyHisPheGlyValArgGluAspProAspPheThr 380
Db 1172 AACAGGTTTTTGAAGACTGCTGCTATGGACATTTTGGAGAGAGACCTGACTTCACA 1231
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
Db 1232 TGGGAAGTGGTCAAAACCCCTCAAGTGGGAGAGGCC 1267

RESULT 15
US-10-425-114-8325
; Sequence 8325, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8325
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700747550_FLI
US-10-425-114-8325

Alignment Scores:
Pred. No.: 3,51e-227 Length: 1461
Score: 2073.00 Matches: 389
Percent Similarity: 99.74% Conservative: 2
Best Local Similarity: 99.23% Mismatches: 1
Query Match: 99.52% Indels: 0
DB: 18 Gaps: 0

US-10-734-698A-39 (1-392) x US-10-425-114-8325 (1-1461)

QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
Db 95 ATGGCAGAGACATTCCTATTACTCAGAGTCCGGTGAACGAGGACACCTTGACAGCTC 154
QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
Db 155 TGGGACCAATCTCCGATGCTGCTCGAGCTTGCTCGAGCAGGACCCAGACACGAAA 214
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
Db 215 GTTGCTCGGAAACATGCACCAAAACCACTTGGTTCATGGTCTTCGGAGAAATCAGGACC 274
QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
Db 275 AAGGCCAACCTTGACTACGAGAGATAGTCGTCACACCTGCAGGAAACATCGGCTTCGTC 334
QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGln 100
Db 335 TCAATGATGTGGACTGGATGGCGCACTGCAAGGTCTCTCAACATTGAGAGAGCAG 394
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120

Db 395 AGCCCTGATATTGCTCAGGGGTGTACACGCGCCACCTTACAAAAAAACCTGAGAAATTTGGT 454
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
Db 455 GCTGTGTGACCAAGGTCACATGTTTGGCTATGCTATGCACTGATGAAACCCCTGAATTGATGCCA 514
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
Db 515 TTGAGCCATGTTCTTTGCAACAAACTCGGTGCTGCTCTCACCGAGGTTTCGCAAGAACCGT 574
QY 161 ThrCysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAsp 180
Db 575 ACCTGCCCTTGGCTGAGGCTGATGGAGAGACCCCAAGTGACCGTTGAGTATTACATGAC 634
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
Db 635 AATGTTGCCAGGGTTCCTATTGCTGTACACACCGTCTAATCTCCACCCCAACACGACGAG 694
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
Db 695 ACTGTCAACCAATGACGAAATTCGTCTGACCTCAAGAGACATGTGATCAAGCCTGTGATC 754
QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
Db 755 CCAGAGAAAGTACCTTGTGATGAGAAAGCAATTTTCCACTTGAACCCCTTCAGGCCGTTTGTTC 814
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
Db 815 ATTGTGCGCCCTCATGCGGATGCTGCTCTCACCGCGCCGCAAGATCATTATCGATACTTAT 874
QY 261 GlyGlyTrpGlyAlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
Db 875 GGAGGATGGGTGCTCATGCTGCTGCTTCTCCGGGAGGACCTTACCAAGGTTGAT 934
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAla 300
Db 935 AGGAGTGGTGTCTTACATTGTGAGACAGGCTGTAAAGAGCATTTGGCAAGTGGACTTGCC 994
QY 301 ArgAspCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
Db 995 AGAAGTGTGATTTGTCGAAGTGTCTTATGCCATTGGTGTGCTGAGCCTTTGCTGTGTTT 1054
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
Db 1055 GTTGACACCTATGGCACTGGGAAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAA 1114
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
Db 1115 AACTTTGATTTTCAGGCTGGTATGATCTCCATCAACCTTGTATCTCAAGAGGGTGGAAAT 1174
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380
Db 1175 AACAGGTTTTTGAAGACTGCTGCTTATGGACATTTTGGAGAGAGACCTGACTTCACA 1234
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
Db 1235 TGGGAAGTGGTCAAAACCCCTCAAGTGGGAGAGGCC 1270

Search completed: September 12, 2005, 23:19:41
Job time : 875 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2083	100.0	1485	4	US-09-424-9788-38	Sequence 38, Appl
2	1985	95.3	1479	4	US-09-424-9788-40	Sequence 40, Appl
3	1953	93.8	2183	4	US-09-424-9788-37	Sequence 37, Appl
4	1946	93.4	1582	4	US-09-424-9788-35	Sequence 35, Appl
5	1900.5	91.2	1353	4	US-09-424-9788-43	Sequence 43, Appl
6	1891.5	90.8	1380	4	US-09-424-9788-41	Sequence 41, Appl
7	1317.5	63.3	1283	3	US-09-318-448-22	Sequence 22, Appl
8	1317.5	63.3	1283	4	US-09-023-655-1371	Sequence 1371, Ap
9	1317.5	63.3	1283	4	US-09-949-016-4188	Sequence 4188, Ap
10	1317.5	63.3	3495	4	US-09-976-594-470	Sequence 470, App
11	1280.5	61.5	1173	4	US-09-248-796A-4152	Sequence 4152, Ap
12	1274.5	61.2	3320	4	US-09-949-016-1787	Sequence 1787, Ap

QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeu 20
DB 74 ATGGCAGAGACATCTCTATTACCTCAGAGTCAGTGAACGAGGACACCTCGACAGCTC 133
QY 21 CysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLys 40
DB 134 TGGCAGCAAACTCTCCGATGCTGCTCGACGCTTGCCTTGAACAGGACCCAGACAGCAAG 193
QY 41 ValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThr 60
DB 194 GTTGCCCTGGCAACATGCAACCAAGACCACTGGTCTATGGTCTTCGGAGAGATCACACC 253
QY 61 LysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheVal 80
DB 254 AAGGCCAAAGTTGACTACGAGAAGATCGTGGTGACACCTGCAGGACATCGCTTCGTC 313
QY 81 SerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 100
DB 314 TCAACGATGTGGGACTTGATGCTGCAACTGCAAGTCTTGTAAACATTGAGCAGCAG 373
QY 101 SerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGly 120
DB 374 AGCCCTGATATTGCCAGGGTGTGACGGCCACCTTACCAGGAGCCCGAGGAAATCGGT 433
QY 121 AlaGlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetPro 140
DB 434 GCTGGAGACCGGTCACATGTTTGGCTATGCCAGGACGAAACCCCAAGATTGATGCCA 493
QY 141 LeuSerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGly 160
DB 494 TTGAGTCATGTTCTTCAACTAACTCGGTGCTCGTCTCACCGAGGTTCCGCAAGAACGGA 553
QY 161 ThrCysProTyrLeuArgProAspGlyLysThrGlnValThrValGluTyrThrAsnAsp 180
DB 554 ACTGTGCCCATGGTTGAGGCTTGATGGGAAACCCCAAGTGACTGTGGAGATTACAAATGAC 613
QY 181 AsnGlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGlu 200
DB 614 AACGGTGCCATGGTTCCAGTTCGTGTCCACACTGTGCTTATCTCCACCCCAACATGATGAG 673
QY 201 ThrValThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIle 220
DB 674 ACTGTGACCAACGACGAAATTGCGTGCATGACCTCAAGGAGCATGTGATCAAGCGGTGATC 733
QY 221 ProGluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheVal 240
DB 734 CCGGAGAGTACTCTGATGAGAAGACCATTTCCACTTGAACCCCTCTGGCCGTTTGTTC 793
QY 241 IleGlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyr 260
DB 794 ATTTGAGGTCCTCACGGTGATGCTGGTCTCACCGGCGCAAGATCATCATCGATACTTAC 853
QY 261 GlyGlyTyrGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAsp 280
DB 854 GGAGGATGGGGTGCTCATGGTGGTGGTCTTCTCCGGGAAGGATCCCAACCAAGGTTGAT 913
QY 281 ArgSerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyValAla 300
DB 914 AGAGTGGTGCTTACATTTGTGAGACAGGCTGCTAGAGCATTTGGCAGTGGAGTACGCC 973
QY 301 ArgArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPhe 320
DB 974 AGAAGGTGCATTTGTCAAGTGCTTATGCCATTGGTGTGCCCGAGCCTTTGTCTCTTT 1033
QY 321 ValAspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGlu 340
DB 1034 GTTGACCATATGGCACCGGGAAGATCCATGATAAGGAGATTCTCAACATTGTGAAGGAG 1093
QY 341 AsnPheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsn 360
DB 1094 AACTTTGATTTTCAAGCCCGGTTATGATCTCCATCAACTTGAATCTCAAGAGGGGTGGGAT 1153
QY 361 AsnArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThr 380

DB 1154 AACAGTTCTTGAAGACTGCTGCATATGCACACTTCGGCAGAGAGACCTGACTTCACA 1213
QY 381 TrpGluValValLysProLeuLysTrpGluLysAla 392
DB 1214 TGGGAAGTGGTCAAGCCCTCAAGTGGGAGAAGGCC 1249
RESULT 2
US-09-424-978B-40
; Sequence 40, Application US/09424978B
; Patent No. 6664445
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Abell, Lynne N.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
; FILE REFERENCE: BB-1087
; CURRENT APPLICATION NUMBER: US/09/424,978B
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 60/048,771
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-424-978B-40
Alignment Scores:
Pred. No.: 1e-228 Length: 1479
Score: 1985.00 Matches: 374
Percent Similarity: 97.69% Conservative: 6
Best Local Similarity: 96.14% Mismatches: 9
Query Match: 95.30% Indels: 0
DB: 4 Gaps: 0
US-10-734-698A-39 (1-392) x US-09-424-978B-40 (1-1479)
QY 3 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 22
DB 123 GAACCTTCTTATTACCTCCGAGTCTGTGAACGAGGCTCACCCAGACAGCTCTGTGAT 182
QY 23 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAla 42
DB 183 CAGATCTCTGATGCGATTTCTTGTATGCTGCTTGTGAGCAAGATCCGAGAGCAAGTTGCA 242
QY 43 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAla 62
DB 243 TGTGAACCTTCACCAAGACCAACTTGGTCTATGGTCTTTGGTGAGATCACCAACCAAGGCT 302
QY 63 AsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsn 82
DB 303 ATTTGAGCATATGAGAGATTGTGGTGACACATGCCGTATATTTGGATTTGTTCTGAT 362
QY 83 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerPro 102
DB 363 GATGTGGTCTTGTATGCTGCAACTGCAAGGTCCTTGTTTACATTGAGCAGCAAGTCTCT 422
QY 103 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyValAlaGly 122
DB 423 GATATTGCTCAAGGTGTCTCACGGCCATCTGACCAAAACCCCGAGGAGATTGGTCTGCT 482
QY 123 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 142
DB 483 GACCAGGGCCACATGTTTGGCTATGCAACACATGAGACCCCTGAAATTAATGCTCTCAGT 542
QY 143 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 162

Db 543 CACGTGCTTCAACTAACTTGGTCCCGCTTACAGAACTCCGCAAGAAATGCACTGC 602
Qy 163 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGly 182
Db 603 GCCTTGTTGAGGCTGATGCAAGACCAAGTTTACTGTTGAGTATAGCAATGCAATGGT 662
Qy 183 AlaMetValProValArgValHisThrValLeuLeuSerThrGlnHisAspGluThrVal 202
Db 663 GCCATGGTTCCAAATAGGTTAGCTACACTGTTCTTATCTCCACCAACACAGTACGACGGTT 722
Qy 203 ThrAsnAspGluLeuAlaAlaAspLeuLysGluHisValIleLysProValIleProGlu 222
Db 723 ACCAATGATGAGATGCGCCGACCTTAAGAGAGATGTCATCAACAGCATCCACAGAG 782
Qy 223 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 242
Db 783 AAGTACCTTCATGAGAATACTATTTCCACCTTAAACCATCTGGCGATTTCGTTATTGGT 842
Qy 243 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 262
Db 843 GGACCTCATGGTATGCTGCTCTCACTGGTCGTAATAATCATCATCGACACTTATGGTGGT 902
Qy 263 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 282
Db 903 TGGGGTGCTCATGGTGGTGGTCTTCTCGGCAAGACCAACCAAGGTCGACAGAGT 962
Qy 283 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg 302
Db 963 GGTGCATACATTGTAAGGCAAGGCTGCAAGAGTATCGTAGCTAGTGGACTTGTCTGTAGA 1022
Qy 303 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 322
Db 1023 TGCATCGTGCAGGTATCTTATGCCATCGGTGTGCTGAGCCATTGCTGTATTCTGTGAC 1082
Qy 323 ThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPhe 342
Db 1083 ACCTATGGCACTCGAAAGATCCCTCAGAGGGAATTTTGAAGATCGTTAAGGAACTTT 1142
Qy 343 AspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnAsnArg 362
Db 1143 GACTTCAGACCTGGAATGATGTCATTAACCTTGATTTGAAGAGGGTGGCAATAGAAG 1202
Qy 363 PheLeuLysThrAlaLysTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGlu 382
Db 1203 TTCTTGAATACTGCTGCTATGCTCACTTTGGACGTGATGACCCCGATTTCATCGGAA 1262
Qy 383 ValValLysProLeuLysTrpGluLys 391
Db 1263 GTTGTCAAGCCCTCAAGTGGGAAAAG 1289

RESULT 3

US-09-424-978B-37
; Sequence 37, Application US/09424978B
; Patent No. 6664445
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafaleki, J. Antoni
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Abell, Lynne N.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
; FILE REFERENCE: BB-1087
; CURRENT APPLICATION NUMBER: US/09/424,978B
; CURRENT FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 60/048,771
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 2183
; TYPE: DNA

; ORGANISM: Oryza sativa
US-09-424-978B-37

Alignment Scores:

Prod. No.: 1-34e-224 Length: 2183
Score: 1953.00 Matches: 364
Percent Similarity: 97.11% Conservatives: 14
Best Local Similarity: 93.57% Mismatches: 11
Query Match: 93.76% Indels: 11
DB: 4 Gaps: 0

US-10-734-698A-39 (1-392) x US-09-424-978B-37 (1-2183)

Qy 3 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 22
Db 800 GATACCTTCTCTTACCTCGGAGTCTGTGAACGAGGGCCACCTGACAAAGCTCTCGAC 859
Qy 23 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAla 42
Db 860 CAAAGTCTCAGATGCTGTGCTTGCCTGCCCTCGCGAGGACCTGACAGCAAGGTCGCT 919
Qy 43 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAla 62
Db 920 TGTGAGACCTGCACCAAGACAAACATGTCATGGTCTTTGGTGAGATCACCACCAAGGCT 979
Qy 63 AsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsn 82
Db 980 AACGTTGATATGAGAAGATTGTCAGGGAGACATGCCGTAAACATCGGTTTGTGTGAGCT 1039
Qy 83 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerPro 102
Db 1040 GATGTCGGTCTCGATGCTGACCAAGGTCCTTGTGAACATCGAGCAGGAGTCCCT 1099
Qy 103 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly 122
Db 1100 GACATTGACAGGTTGTCACGGGCACTTCACCAAGGCGCTGAGGAGATTGGTGTGCT 1159
Qy 123 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 142
Db 1160 GACCAGGACACATGTTGGATATGCACTGATGAGACCCCTGAGTTGATGCCCTCAGC 1219
Qy 143 HisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCys 162
Db 1220 CATGTCCTTGTACCAAGCTTGGCTGCTCTTACGAGGTTTCGCAAGAAATGGGACCTGC 1279
Qy 163 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGly 182
Db 1280 GCATGGCTCAGGCTGACGGGAAGACCAAGTACTGTTAGTACCGCAATGAGAGCGGT 1339
Qy 183 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 202
Db 1340 GCCAGGGTCCCTGTCCTGTCACACCGCTCTCTATCTTACCCAGCATGATGAGACAGTC 1399
Qy 203 ThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGlu 222
Db 1400 ACCAAGCATGAGATTGCTGCTGACCTGAAGGAGCATGTCATCAAGCCTGTCTATCCCGAG 1459
Qy 223 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 242
Db 1460 CAGTACCTTGTATGAGAGACAACTCTTCCATCTTAACCCATCTGGTCTGCTTCATTGGC 1519
Qy 243 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGly 262
Db 1520 GGACCTCATGTTGATGCTGCTCTCACTGCCCGGAAGATCATCATTTGACACTTATGTTGTC 1579
Qy 263 TrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSer 282
Db 1580 TGGGAGCTCACGGTGGTGGTCTTCTCTGCAAGGACCCCAACCAAGGTTTACCGCAGT 1639
Qy 283 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg 302
Db 1640 GGAGCATATGTCGCAAGGCAAGCTGTCAGAGACATTTGTTGCTAGTGGCTTCTGCTGCGCG 1699

QY 303 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 322
 Db 1700 TGCATTGTCCAGTATCATACGCCATCGGTGTCCAGAGCCACTGTCCGTATTGTCGAC 1759
 QY 323 ThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPhe 342
 Db 1760 ACATACGGCACTGGCAGGATCCCTGACAAAGGAGATCCTCAAGATTGTGAAGGAGAACTTC 1819
 QY 343 AspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyClyAsnAsnArg 362
 Db 1820 GACTTCAGGCCCTGGCATGATCATCAACCTTGACCTCAAGAAAGGGCGCAACGAGCGC 1879
 QY 363 PheLeuLysThrAlaAlaTyrGlyHisPheGlyValGluAspProAspPheThrTrpGlu 382
 Db 1880 TACCTCAAGACGGCGGCTTACGGTCACTTCGGNAGGGAGACCCAGACTTCACTTGGGAG 1939
 QY 383 ValValLysProLeuLysTrpGluLys 391
 Db 1940 GTGGTGAAGCCCTCAAGTGGGAGAAG 1966

RESULT 4

US-09-424-978B-35
 ; Sequence 35, Application US/09424978B
 ; Patent No. 6664445
 ; GENERAL INFORMATION:
 ; APPLICANT: Falco, Saverio Carl
 ; APPLICANT: Allen, Stephen M.
 ; APPLICANT: Rafalski, J. Antoni
 ; APPLICANT: Hitz, William D.
 ; APPLICANT: Kinney, Anthony J.
 ; APPLICANT: Abell, Lynne N.
 ; APPLICANT: Thorpe, Catherine J.
 ; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
 ; FILE REFERENCE: BB-1087
 ; CURRENT APPLICATION NUMBER: US/09/424,978B
 ; CURRENT FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: US 60/048,771
 ; PRIOR FILING DATE: 1997-06-06
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 35
 ; LENGTH: 1582
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 US-09-424-978B-35

Alignment Scores:

Pred. No.: 5,56e-224 Length: 1582
 Score: 1946.00 Matches: 363
 Percent Similarity: 96.92% Conservative: 14
 Best Local Similarity: 93.32% Mismatches: 12
 Query Match: 93.42% Indels: 0
 DB: 4 Gaps: 0

US-10-734-698A-39 (1-392) x US-09-424-978B-35 (1-1582)

QY 3 GluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAsp 22
 Db 152 GACACCTTCTCTTCACTCGAGTGTGTGAACGAGGGACACCTGACAAGCTCTGCGAC 211
 QY 23 GlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAla 42
 Db 212 CAGGTCTCAGATGCCGTCTTTCAGCGCTTGCTTGTGAGGACCTGACAGCAAGTGTCT 271
 QY 43 CysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAla 62
 Db 272 TGTGAGACCTGCACCAAGACCAACATGGTGTATGGTCTTGTGAGATCACCACCAAGGCC 331
 QY 63 AsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsn 82
 Db 332 AATGTCGACTACGAGAAGATTGTGAGGAGACCTGCCGCAACATGGTGTGTGTGTCAAAC 391
 QY 83 AspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnSerPro 102

Db 392 GATGTCGGGCTTGACGCTGACCACTGCAAGGTGCTCGTGAACATTGACGACAGTCCCT 451
 QY 103 AspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGly 122
 Db 452 GATATTGCTCAGGGTGTGCATGGCCACTTCCCAAGCGCCCGGAGAGATTGGAGCTGT 511
 QY 123 AspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSer 142
 Db 512 GACCAAGGACACATGTTCCGGGTATGCGACCGATGAGACCCCTGAGTTGATGCCCTCAGC 571
 QY 143 HisValLeuAlaThrLysLeuGlyValAlaArgLeuThrGluValArgLysAsnGlyThrCys 162
 Db 572 CATGTCCTTGCACCAACCTAGGTGCTGCTCTACCGAGGTCCGCAAGACGGAACCTGC 631
 QY 163 ProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGly 182
 Db 632 CCTGGCTCAGGCTGTATGGGAAGACCCAGGTGACAGTCGAGTACCCGAATGAGGGTGT 691
 QY 183 AlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrVal 202
 Db 692 GCCATGGTCCCATCCGTGTCACACCGTCTCTCATCTCCACCAGACGACGAGACAGTG 751
 QY 203 ThrAsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGlu 222
 Db 752 ACCAATGATGAGATCGCTGCTGACCTGAAGGAGCATGTCATCAAGCCTATCATCCTCG 811
 QY 223 LysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 242
 Db 812 CAGTACCTTTGACGAGAACCATCTTCCACCTTAACCCATCCGCCGCTTTGTCTATTGT 871
 QY 243 GlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGly 262
 Db 872 GGACCTCAGCGGATGCTGGCTCTACTGGCCGCAAGATCATCATTTGACACCTACGCTGC 931
 QY 263 TrpGlyAlaHisGlyGlyValAlaPheSerGlyLysAspProThrLysValAspArgSer 282
 Db 932 TGGGAGGCCCATGCGGTGGCGCTTTCTCCGCAAGGAGACCACCAAGGTTGACCGCAGC 991
 QY 283 GlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArgArg 302
 Db 992 GGAGCCTATGTGCGAGGACGAGCTGCCAAGAGCATGCTGCGCAGCGGCTTGTCTCGCGC 1051
 QY 303 CysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAsp 322
 Db 1052 GCCATCGTCCAGGTGCTCTACGCATCGCGCTGCGGAGCCTCTCTCGTGTGTCGAC 1111
 QY 323 ThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPhe 342
 Db 1112 ACGTAGGCGCACCGCGCGATCCCGACAAGGAGATCCTCAAGATTGTCAAGGAGAACTTC 1171
 QY 343 AspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyClyAsnAsnArg 362
 Db 1172 GATTTCAGGCTGCGCATGATTATCATCAACCTTGACCTCAAGAAAGGGCGCAACGGGCGC 1231
 QY 363 PheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGlu 382
 Db 1232 TACCTCAAGCGGACGCTACGCCACTTCGGAAGGGAGACCCCTGACTTCACTTGGGAG 1291
 QY 383 ValValLysProLeuLysTrpGluLys 391
 Db 1292 GTGGTGAAGCCACTCAAGTCGGAGAAA 1318

RESULT 5

US-09-424-978B-43
 ; Sequence 43, Application US/09424978B
 ; Patent No. 6664445
 ; GENERAL INFORMATION:
 ; APPLICANT: Falco, Saverio Carl
 ; APPLICANT: Allen, Stephen M.
 ; APPLICANT: Rafalski, J. Antoni
 ; APPLICANT: Hitz, William D.
 ; APPLICANT: Kinney, Anthony J.

RESULT 6

US-10-734-698A-39 (1-392) x US-09-424-978B-41 (1-1380)

Db 79 GCCGAGACGTTCCCTCTTCAAGTCCGAGTCTGTGAACGAGGGCCATCCCGACAAGCTCTGT 138

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QY 22 AspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysVal 41
Db 139 GACCAAGTCTCGACCGCGTCTTGGATGCTTGGCCAGAGTCCACACAGCAGGTC 198
QY 42 AlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLys 61
Db 199 GCCTGGACCGCTCACCAAGACCAACATGATGGTCTTGGCGAGATCACCAACAG 258
QY 62 AlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSer 81
Db 259 GCCACCGTCGACTATGAGAAGATCGTGCCTGACACCTGCCGGAACATCGTTCTCT 318
QY 82 AsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnSer 101
Db 319 GATGACGTTGGTCTCGACCGCCAGCCGTTGCAARGTCTGTCACATCGAGCAGATCC 378
QY 102 ProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAla 121
Db 379 CCTGACATTCGCCAGGCTGTCATGCACACTTCACCAAGCGTCCCGAAGAGTCGGCG 438
QY 122 GlyAspGlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeu 141
Db 439 GGTGACCGGATCATGTTGCGCTATGCCCGCATGCCAGTGCAGCCCTGAGCTGATGCC 498
QY 142 SerHisValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThr 161
Db 499 AGCAGCTGCTTGCACCAAGCTYGAGCTCGCTCACGAGTCCGCAAGATGTCACCC 558
QY 162 CysProTrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsn 181
Db 559 TCGCGCTGGTCCAGGCTCAGCGAAGAGCCAGGTCACAGTCGAGTACCTAAACAGGAT 618
QY 182 GlyAlaMetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThr 201
Db 619 GGTGCCATGATGATCTTCTGCTGTCACACCGCTCTCATCTCCACCGACACGACGAG 678
QY 202 ValThrAsnAspGluIleAlaLeuAspLeuLysGluHisValIleLysProValIlePro 221
Db 679 GTCCACCAAGCAGAGATGCTCGGACCTCAAGGACGATGTATCAAGCCGGTGATCCCC 738
QY 222 GluLysTyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIle 241
Db 739 GCAAAGTACCTCGATGAGAACCCTCTTCCACCTGAAACCGCTCTGGCGCTTCGTATC 798
QY 242 GlyGlyProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGly 261
Db 799 GCGCGCCCCCAGCGTGACCGCGTCTCACCGCCGCAAGATCATCATCGACACCTATG 858
QY 262 GlyTrpGlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArg 281
Db 859 GGTGGGGAGCCACCGCGCGGTGCTTCTTGGCAAGGACCCAAACCAAGGTGACCGY 918
QY 282 SerGlyAlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArg 301
Db 919 AGTGGCGCTACATGCCCAGGARGCGCCCAAGAGCATCATGCCAGCGCGCTCGCACGC 978
QY 302 ArgCysIleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheVal 321
Db 979 CGCTGCATTTGTCAGATCTCATACGCCATCGGTGTGCTGAGCCCTTGTGTGTCGTC 1038
QY 322 AspThrTyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsn 341
Db 1039 GACTCTCAGGCNCCGGCAAGATCCCGACAGGGAGATCCTCAAGCTCGTGAAGGAGAAC 1098
QY 342 PheAspPheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnAsn 361
Db 1099 TTTGACTTCAGGCCCGGGATGATCAGATCAACCTGGACTTGAAGAAAGGTGGA---AAC 1155
QY 362 ArgPheLeuLysThrAlaIaTyrGlyHisPheGlyArgGluAspProAspPheThrTrp 381
Db 1156 AGTTTCATCAAGACCGCTCTTACGGTCACTTTGGCCGTCGATGATGCCGACTTCACCTGG 1215
QY 382 GluValValLysProLeuLysTrpGluLysAla 392
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Db 1216 GAGGTGGTGAAGCCCTCAAGTTCGACACAGGCA 1248
RESULT 7
US-09-318-448-22
; Sequence 22, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Stenroos, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1283
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-22
Alignment Scores:
Pred. No.: 1,97e-148 Length: 1283
Score: 1317.50 Matches: 255
Percent Similarity: 78.35% Conservative: 49
Best Local Similarity: 65.72% Mismatches: 77
Query Match: 63.25% Indels: 7
DB: 3 Gaps: 3
US-10-734-698A-39 (1-392) x US-09-318-448-22 (1-1283)
QY 4 ThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAspGln 23
Db 114 ACATTCTCTTTTCCACTCAGAGTCGGTCGGGAAGGCCACCACGATAGATTGTGACCAA 173
QY 24 IleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAlaCys 43
Db 174 ATCAGTGATGCTGCTCTTGATGCCACCCTTCAGCAGGATCCTGTGACCAAGATGCTTGT 233
QY 44 GluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAlaAsn 63
Db 234 GAACTGTTGTATAAACTGGAATGATCTCTTGTCTGGGAAATTTACATCCAGAGCTGCT 293
QY 64 ValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsnAsp 83
Db 294 GTTGACTACCAAGAGTGGTTCGTGAAGCTGTGTTAAACACATTTGGATATGATGATTCTTCC 353
QY 84 ValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerProAsp 103
Db 354 AAAGTTTTTGACTCAAGACTTTGTAACGTGCTGGTAGCTTGGAGCAACAGTCACAGAT 413
QY 104 IleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGlyAsp 123
Db 414 ATTGCTCAAGGTGTT-----CATCTGCACAAATGAAGAAGACATTGGTCTCGAGAC 467
QY 124 GlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHis 143
Db 468 CAGGCTTTAATGTTTGGCTATGCCACTGATGAACTGAGGAGTGTATGCTTTAACCACT 527
QY 144 ValLeuAlaThrLysLeuGlyValArgLeuThrGluValArgLysAsnGlyThrCysPro 163
Db 528 GTCCTGGGCACCAAGCTAAATGCCAATGCGCAGAACCTACGCCGTAATGGCACTTGGCT 587
QY 164 TrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGlyAla 183
Db 588 TGGTTACGCCCTGATTCATAAACTCAAGTTACTGTGCAGTATATGCAGATCGAGTGTCT 647
QY 184 MetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrValThr 203
Db 648 GTGCTTCCCATCAGATGCCACACAAATTTGTTATCTGTTTCAGCATGATGATGAAGAGTGT 707
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Qy 204 AsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGluLys 223
Db 708 CTTGATGAATGAGGATGCCCTAAAGGAGAAAGTCATCAAGCAGTTGTGCTCGCAAA 767
Qy 224 TyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 243
Db 768 TACCTTGATGAGATACATCTTACCCTACGCAAGTGGCAGATTGTTATGTGGG 827
Qy 244 ProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGlyTyr 263
Db 828 CCTCAGGCTGATGCTGTTGCTGACGCGGAAATCATTTGTGACACATTATGCGGTGG 887
Qy 264 GlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSerGly 283
Db 888 GGTGCTCATGAGGAGTGCTTTTCAGGAAGGATTATACCAAGGTCGACCGTTTCAGCT 947
Qy 284 AlaTyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArgArgCys 303
Db 948 GCTTATGCTGCTGTTGGTGGGCAAAATCCCTGTTAAAGGAGGTCGTGCGGAGGGTT 1007
Qy 304 IleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAspThr 323
Db 1008 CTTGTTCAAGTCTCTATGCTATGAGTTTCTCATCCATTATCTATCTCCATTTCCAT 1067
Qy 324 TyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluLysAsnPheAsp 343
Db 1068 TATGGTACCTCTCAGAAGAGTGAGAGAGAGCTATTAGAGATTGTGAAGAAGATTTCGAT 1127
Qy 344 PheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPhe 363
Db 1128 CTCGCGCTGGGTGCTATGTCAGGAGTCTGGATCTGAAGAAG-----CCAATTAT 1178
Qy 364 LeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTyrGluVal 383
Db 1179 CAGAGACTGACGCTATGCGCACTTGTGTAGGAC-----AGCTTCCATCGGAAGTG 1232
Qy 384 ValLysProLeuLysTrpGluLys 391
Db 1233 CCCAAAAAGCTTAAATATTGAAAG 1256

RESULT 8
US-09-023-655-1371
Sequence 1371, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
```

```
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1371:
SEQUENCE CHARACTERISTICS:
LENGTH: 1283 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g36326
US-09-023-655-1371

Alignment Scores:
Pred. No.: 1,97e-148 Length: 1283
Score: 1317.50 Matches: 255
Percent Similarity: 78.35% Conservative: 49
Best Local Similarity: 65.72% Mismatches: 77
Query Match: 63.25% Indels: 7
DB: 4 Gaps: 3

US-10-734-698A-39 (1-392) x US-09-023-655-1371 (1-1283)
Qy 4 ThrPheLeuPheThrSerGluSerValAlaAsnGluGlyHisProAspLysLeuLysAspGln 23
Db 114 ACATTCCTTTTTCACCTCAGAGTCGTCGCGGAGGCCACCCAGATAGATTGTGACCAA 173
Qy 24 IleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAlaCys 43
Db 174 ATCAGTGTATGCTGCTCTTGTATGCCACCTTCAGCAGGATCCTGATGCCAAAGTAGCTGT 233
Qy 44 GluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAlaAsn 63
Db 234 GAACTGTGTCTAAACTGGAATGATCTCTTCTGCTGGGAAATTTACATCCAGAGCTGT 293
Qy 64 ValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsnAsp 83
Db 294 GTTGACTACCAAGAGTGTGCTGAGCTGTTAAACACATTTGATATGATGATCTTCTCC 353
Qy 84 ValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerProAsp 103
Db 354 AAAGGTTTGTACTACAAGACTTGTAACTGCTGTGTAGCTTTGGAGCAACAGTCACCAT 413
Qy 104 IleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGlyAsp 123
Db 414 ATTGCTCAAGGTGTT-----CATCTTGACAAATGAAGAAGACATTTGGTCTCGAGAC 467
Qy 124 GlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHis 143
Db 468 CAGGCTTAATGTTTGGCTATGCCACTGATGAACTGAGGAGTGTATGCTTTTACCATT 527
Qy 144 ValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCysPro 163
Db 528 GTCTTGGCACCAAGCTAAATGCCAACTGGCAGAACTAGCCCGTAATGGCACTTTGCT 587
Qy 164 TrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGlyAla 183
Db 588 TGGTTACGCCCTGATTTCTAAACTCAAGTTACTGTGCAGTATATGCAGGATCGAGTGT 647
Qy 184 MetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrValThr 203
Db 648 GTGCTTCCCATCAGAGTCCACAAATTTGTTATCTGTTTACGATGATGAAGAGTTTGT 707
Qy 204 AsnAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGluLys 223
Db 708 CTTGATGAATGAGGATGCCCTAAAGGAGAAAGTCATCAAGCAGTTGTGCTCGCAAA 767
Qy 224 TyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGly 243
Db 768 TACCTTGATGAGATACATCTTACCACCTACAGCAAGTGGCAGATTGTTTATTGTTGGT 827
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QY 244 ProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyTyr 263
Db 828 CCTCAGGGTGATGCTGGTTGACTGGACGGAAATCATTTGGACACTTATGGCGGTGG 887
QY 264 GlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSerGly 283
Db 888 GGTGCTCATGGAGGAGTCCCTTTTCAGGAAGGATTATACCAAGGTCGACCGTTCAGCT 947
QY 284 AlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAlaArgCys 303
Db 948 GCTTATGCTGCTCGTTGGGTGGCAAAATCCCTTTTAAAGGAGGTCGTGCGCGAGGGTT 1007
QY 304 IleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAspThr 323
Db 1008 CTTGTTTCAGGTCCTTATGCTATGGAGTTTCTCATCCATTATCATCTCCATTTTCCAT 1067
QY 324 TyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPheAsp 343
Db 1068 TATGGTACCTTCAGGAAGAGTGAGAGAGCTATTAGAGATTGTGAAGAAGATTTCGAT 1127
QY 344 PheArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPhe 363
Db 1128 CTCGCGCCCTGGGGTCATTGTCGGGATCTGGATCTCAAGAAG-----CCAATTAT 1178
QY 364 LeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGluVal 383
Db 1179 CAGAGAGCTGCAGCCTATGGCCACTTTGGTAGGGAC-----AGCTTCCATCGGGAAGTG 1232
QY 384 ValLysProLeuLysTrpGluLys 391
Db 1233 CCCAAAAAGCTTAATATTGAAAG 1256
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RESULT 9

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US-09-949-016-4188
; Sequence 4188, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIORITY FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIORITY FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: fastseq for windows version 4.0
; SEQ ID NO 4188
; LENGTH: 1283
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4188
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Alignment Scores:
Pred. No.: 1.97e-148 Length: 1283
Score: 1317.50 Matches: 255
Percent Similarity: 78.35% Conservative: 49
Best Local Similarity: 65.72% Mismatches: 77
Query Match: 63.25% Indels: 7
DB: 4 Gaps: 3
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US-10-734-698A-39 (1-392) x US-09-949-016-4188 (1-1283)

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QY 4 ThrPheLeuPheThrSerGluSerValAsnGlnGlyHisProAspLysLeuCysAspGln 23
Db 114 ACATTCCCTTTTCACTCTCAGAGTCGGTCGGGGAAGGCCACCCAGATAAGATTGTGACCAA 173
QY 24 IleSerAspAlaValLeuAspAlaCysLeuGlnAspProAspSerLysValAlaCys 43
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Db 174 ATCAGTGATGCTGCTTGTGATGCCACCTTCAGCAGGATCCTGATGCCAAAGTAGCTTGT 233
QY 44 GluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAlaAsn 63
Db 234 GAAACTGTTGCTAAAACTGGAATGATCCTTCTTGTCTGGGAAATTTACATCCAGAGCTGCT 293
QY 64 ValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsnAsp 83
Db 294 GTTGACTACCAAGAAAGTGGTTGCGAAGCTGTTAAACACATTTGGATATGATGATTCTTCC 353
QY 84 ValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerProAsp 103
Db 354 AAAGGTTTTGACTACAGACTTGTAACTGCTGGTAGCTTGGAGCAACAGCTCACCAGAT 413
QY 104 IleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGlyAsp 123
Db 414 ATTGCTCAAGGTGTT-----CATCTTCAGCAAAATGAAGAAGACATTTGGTCTGGAGAC 467
QY 124 GlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHis 143
Db 468 CAGGCTTTAAATGTTTGGCTATGCCACTGATGAAACTGAGGAGTGTATGCTTTAAACCAT 527
QY 144 ValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCysPro 163
Db 528 GTCCTGGCACACNAGCTAAATGCCAACTGGCAGAACTACGCCGTAATGGCACTTTGCCT 587
QY 164 TrpLeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGlyAla 183
Db 588 TGGTTACGCCCTGATTCTTAAAACTCAAGTTACTGTGTCAGTATATGCAGGATCGAGGTGCT 647
QY 184 MetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrValThr 203
Db 648 GTGCTTCCCATCAGAGTCCACAAATTTGTATATCTGTTACGATGATGAAGAGTTTGT 707
QY 204 AsnAspGluIleAlaAlaAspLysGluHisValIleLysProValIleProGluLys 223
Db 708 CTTGATGAATGAGGATGCCCTTAAAGGAGAAAGTCATCAAGAGCTTGTGCTCGCGAAA 767
QY 224 TyrLeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGlyGly 243
Db 768 TACCTTGATGAGGATACAAATCTACCACCTACAGCCAAGTCGACAGATTTGTTATTGGTGG 827
QY 244 ProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyGlyTrp 263
Db 828 CCTCAGGGTGATGCTGGTTTGAACGCAAAATCATTTGGACACACTTATGGCGGTGG 887
QY 264 GlyAlaHisGlyGlyValAlaPheSerGlyLysAspProThrLysValAspArgSerGly 283
Db 888 GGTGCTCATGGAGGAGTGCCTTTTCAGGAAGGATTATACCAAGGTCGACCGTTCAGCT 947
QY 284 AlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAlaArgArgCys 303
Db 948 GCTTATGCTGCTCGTTGGGTGGCAAAATCCCTTTTAAAGGAGGTCGTGCGCGAGGGTT 1007
QY 304 IleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAspThr 323
Db 1008 CTTGTTTCAGGTCCTTATGCTATGGAGTTTCTCATCCATTATCATCTCCATTTTCCAT 1067
QY 324 TyrGlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPheAsp 343
Db 1068 TATGGTACCTTCAGGAAGAGTGAGAGAGCTATTAGAGATTGTGAAGAAGAAATTTCCAT 1127
QY 344 PheArgProGlyMetIleSerIleAsnLeuAspLysArgGlyGlyAsnAsnArgPhe 363
Db 1128 CTCGCGCCCTGGGGTCATTGTCAGGAGTCTGATCTGAAGAAG-----CCAATTAT 1178
QY 364 LeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGluVal 383
Db 1179 CAGAGAGCTGCAGCCTATGGCCACTTTGGTAGGGAC-----AGCTTCCATCGGGAAGTG 1232
QY 384 ValLysProLeuLysTrpGluLys 391
Db 1233 CCCAAAAAGCTTAATATTGAAAG 1256
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Db 1233 CCCAAAAAGCTTAAATATTGAAG 1256

RESULT 10

US-09-976-594-470

; Sequence 470, Application US/09976594

; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 470

; LENGTH: 3495

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6673549 2600262CB1

; NAME/KEY: unsure

; LOCATION: 2831-2993

; OTHER INFORMATION: a, t, c, g, or other

US-09-976-594-470

Alignment Scores:

Pred. No.: 9,97e-148 Length: 3495

Score: 1317.50 Matches: 255

Percent Similarity: 78.35% Conservative: 49

Best Local Similarity: 65.72% Mismatches: 77

Query Match: 63.25% Indels: 7

DB: 4 Gaps: 3

US-10-734-698A-39 (1-392) x US-09-976-594-470 (1-3495)

QY 4 ThrPheLeuPheThrSerGluSerValAenGluGlyHisProAspLysLeuCysAspGln 23

Db 163 ACATTCTTTTCACTCAGAGTCGGTGGGAAGGCCACCCAGATGAATTTGTGACCAA 222

QY 24 IleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAlaCys 43

Db 223 ATCAGTGATGCTGCTCTTGATGCCACCTTCAGCAGATCCTGATGCCAAAGTAGCTGT 282

QY 44 GluThrCysThrLysThrAenLeuValMetValPheGlyGluIleThrThrLysAlaAen 63

Db 283 GAAACTGTTGTCTAAACTGGAATGATCTCTTCTGCTGGGGAATTTATCATCCAGAGCTGCT 342

QY 64 ValAspTyrGlyLysIleValArgAspThrCysArgAenIleGlyPheValSerAenAsp 83

Db 343 GTTGACTACCAAGAGTGTCTGAGCTGTTAAACACATGGATATGATGATTTCTTC 402

QY 84 ValGlyLeuAspAlaAspAenCysLysValLeuValAenIleGluGlnSerProAsp 103

Db 403 AAAGGTTTGGACTACAGACTTGTAACTGCTGAGCTGTGGAGCAACAGTCCACAGAT 462

QY 104 IleAlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGlyAsp 123

Db 463 ATTGCTCAAGGTGTT-----CATCTTGACAGAAATGAAGACACATTTGCTGGAGAC 516

QY 124 GlnGlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHis 143

Db 517 CAGCGCTTAATGTTGGCTATGCCACTGATGAACCTGAGAGTGTATGCTTTAACATT 576

QY 144 ValLeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAenGlyThrCysPro 163

Db 577 GTCTTGGCACACAGCTAAATGCCAACTGGCAGAACTAGCCGCTAATGGCACTTTGCT 636

QY 164 TrpLeuArgProAspGlyLysThrGlnValThrValGluTyrThrAenAspAenGlyAla 183

Db 637 TGGTTACGCCCTGATTCTAAACTCAAGTTACTGTGCAGTATATGTCAGGATCAGGTGCT 696

QY 184 MetValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrValThr 203

Db 697 GTGCTTCCCATCAGAGTCCACAAATTGTTATATCTGTTCCAGCATCATGAAGAGTTGT 756

QY 204 AenAspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGluLys 223

Db 757 CTTGATGAATGAGGAGTCCCTTAAAGGAGAAAGTCAATCAAGAGCATTGTGCTCGCAA 816

QY 224 TyrLeuAspGluLysThrIlePheHisLeuAenProSerGlyArgPheValIleGlyGly 243

Db 817 TACCTTGTAGAGATACAATCTACCACTACAGCAAGTGGCAGATTGTTATTTGGTGG 876

QY 244 ProHisGlyAspAlaGlyLeuThrGlyArgLysIleIleIleAspThrTyrGlyGlyTyr 263

Db 877 CCTCAGGTTGATGCTGTTTGTGTCGACGGAATAATCATTTGTGACACTTATGCGGTTGG 936

QY 264 GlyAlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSerGly 283

Db 937 GGTGCTCATGAGGAGTGCCTTTTCAGGAAAGGATTATACCAAGGTCGACCGCTTCAGCT 996

QY 284 AlaTyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAlaArgArgCys 303

Db 997 GCTTATGCTGCTGTTGGTGGCAAAATCCCTTTTAAAGGAGGTCTGTGCCGAGGGTT 1056

QY 304 IleValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAspThr 323

Db 1057 CTTGTTCAAGTCTCTTATGCTATTTGGAGTTTCTCATCCATTATCTATCTCCATTTTCCAT 1116

QY 324 TyrGlyThrGlyLysIleHisAspLysGluIleLeuAenIleValLysGluAenPheAsp 343

Db 1117 TATGTTACCTCTCAGAAAGTGCAGAGAGCTATTAGAGATTGTGAAGAAGAAATTTTCGAT 1176

QY 344 PheArgProGlyMetIleSerIleAenLeuAspLeuLysArgGlyGlyAenAenArgPhe 363

Db 1177 CTCGCCCTGGGGTCAATGTCAGGGATCTGGATCTGAAGAAG-----CCAAATTTAT 1227

QY 364 LeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGluVal 383

Db 1228 CAGAGGACTGCAGCTTATGCCACATTTGTTGGAGGAC-----AGCTTCCCATGGGAAGTG 1281

QY 384 ValLysProLeuLysTrpGluLys 391

Db 1282 CCCAAAAAGCTTAAATATTGAAG 1305

RESULT 11

US-09-248-796A-4152

; Sequence 4152, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstein et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 4152

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Candida albicans

US-09-248-796A-4152

Alignment Scores:

Pred. No.: 4,88e-144 Length: 1173

Score: 1280.50 Matches: 242

Percent Similarity: 77.00% Conservative: 56

Best Local Similarity: 62.53% Mismatches: 82


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Db 477 GGTGGTGGTTCGGCTATGCTACCGACGACGACGAGGATGCGATGCCCTCCACCATCATC 536
Qy 145 LeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCysProTyrP 164
Db 537 CTGTGCTCACAGCTCAACGCCGGATGGCAGACCTCAGGCGCTCCGGCTCTCCCTCGG 596
Qy 165 LeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGlyAlaMet 184
Db 597 CTGCGGCTGACTCTAAGACTCAGGTGACAGTTTCTAGTACATGATGACGACAAATGGCGAGTC 656
Qy 185 ValProValArgValHisThrValLeuLeuSerThrGlnHisAspGluThrValThrAsn 204
Db 657 ATCCCTGTGGCATCCACCATCTCTGTGCGACACCAAGACATCATCGCTG 716
Qy 205 AspGluAlaAlaAspLeuLysGluHisValIleLysProValIleProGluLysTyr 224
Db 717 GAGGAGATGCGGCGCTTCAAGAGCAAGTATCATCGGCGCGTGTGCGGCCAAGTAC 776
Qy 225 LeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGlyPro 244
Db 777 CTGGACGAAGACACCGCTCTACCACTGCGACCGCCAGTGGCGGTGTCATCGGAGGTGCC 836
Qy 245 HisGlyAspAlaGlyLeuThrGlyArgLysValIleLeuAspThrTyrGlyTyrGly 264
Db 837 CAGGGGATGCGGGTGTCTGCTGCCCTGATGATTTATTTGTCACCTATGCGGCTGGGG 896
Qy 265 AlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSerGlyAla 284
Db 897 GCTCATGTGTGGGGCTTCTCTGGGAAGGACTACACCAAGGTGGACCGCTCAGCTGCA 956
Qy 285 TyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAlaArgCysIle 304
Db 957 TATGCTGCCCGCTGGTGGCCAAAGTCTCTGGTGAAGCAGGGCTCTGCCGAGAGTGT 1016
Qy 305 ValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAspThrTyr 324
Db 1017 GTCCAGGTTCTTATCCCATGTTGTTGGCGGCGCTGTCATTTCCATCTTCCACCTAC 1076
Qy 325 GlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPheAspPhe 344
Db 1077 GGNACCTCTCAGNAGACAGCGAGCTGCTGGATGTTGTCATAAGAACTTCGACCTC 1136
Qy 345 ArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeu 364
Db 1137 CGCGCGGCGCTATTGTCAGGATTTGGACTTGAAGAAG-----CCCATCTACCAG 1187
Qy 365 LysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGluValVal 384
Db 1188 AAGACAGCATGCTATGGCCATTTCCGAAGAAGC-----GAGTTCCCATGGGAGGTTC 1241
Qy 385 LysProLeu 387
Db 1242 AGAAGCTT 1250

RESULT 13
US-09-318-448-20
; Sequence 20, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Stenroos, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 3228
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-20
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Alignment Scores:

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Pred. No.: 1.32e-142 Length: 3228
Score: 1274.50 Matches: 241
Percent Similarity: 78.85% Conservative: 61
Best Local Similarity: 62.92% Mismatches: 74
Query Match: 61.19% Indels: 7
DB: 3 Gaps: 3
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US-10-734-698A-39 (1-392) x US-09-318-448-20 (1-3228)

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Qy 5 PheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAspGlnIle 24
Db 123 TTTCATGTTTCACATCCGAGTCTGTGGAGAGGGACACCCGGATAAAGATCTGTACCAGATC 182
Qy 25 SerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAlaCysGlu 44
Db 193 AGTGATGACAGTGTGGATGCCCATCTCAAGCAGACCCCAATGCCNAGGTGGCTGTGAG 242
Qy 45 ThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAlaAsnVal 64
Db 243 ACAGTGTGCAAGACCGCATGCTGCTGTGTGTGAGATCACCTCAATGGCCATGGTG 302
Qy 65 AspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsnAspVal 84
Db 303 GACTACACGCGGTGTGAGGACACCATCAAGCACATCGGCTACGATGACTCAGCCAAAG 362
Qy 85 GlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerProAspIle 104
Db 363 GCTTTGATCTCAAGACTGTCACGCTGTGTGGCTTTGGAGCAGCAATCCCCAGATAT 422
Qy 105 AlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGlyAspGln 124
Db 423 GCCCAGTGGCTC-----CATCTGCACAGAAATAGGAGGATGTGGGGCAGGAGATCAG 476
Qy 125 GlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHisVal 144
Db 477 GCTTTGATGTTTGGCTATGTCTACCGACGACAGAGGAGTGCATCCCTCCACCATCATC 536
Qy 145 LeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCysProTyr 164
Db 537 CTGTGCTCAGACTCAACGCCGGATGGCAGACCTCAGGCGCTCCGGCTCTCCCTCGG 596
Qy 165 LeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGlyAlaMet 184
Db 597 CTGCGGCTGACTCTAAGACTCAGGTGACAGTTTCAAGTACATGTCAGGACAAATGGCGAGTC 656
Qy 185 ValProValArgValHisThrValLeuLeuSerThrGlnHisAspGluThrValThrAsn 204
Db 657 ATCCCTGTGGCATCCACCATCTCTGTGCGACACCAAGACATCATCGCTG 716
Qy 205 AspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGluLysTyr 224
Db 717 GAGGAGATGCGGCGCTTCAAGAGCAAGTATCATCGGCGCGTGTGCGGCCAAGTAC 776
Qy 225 LeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGlyPro 244
Db 777 CTGGACGAAGACACCGCTCTACCACTGCGACCGCCAGTGGCGGTGTCATCGGAGGTGCC 836
Qy 245 HisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyTyrGly 264
Db 837 CAGGGGATGCGGGTGTCTGCTGCCCTGATGATTTATTTGTCACCTATGCGGCTGGGG 896
Qy 265 AlaHisGlyGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSerGlyAla 284
Db 897 GCTCATGTGTGGGGCTTCTCTGGGAAGGACTACACCAAGGTAGACCGCTCAGCTGCA 956
Qy 285 TyrIleValArgGlnAlaLysSerIleValAlaSerGlyLeuAlaArgCysIle 304
Db 957 TATGCTGCCCGCTGGTGGCCAAAGTCTCTGGTGAAGCAGGGCTCTGCCGAGAGTGT 1016
Qy 305 ValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAspThrTyr 324
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Db 1017 GTCCAGGTTTCCTATGCCATTGGTGGCCGAGCGCGTGTCCATTTCCATCTTCCACCTAC 1076
Qy 325 GlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPheAspPhe 344
Db 1077 GGAACCTCTCAGAAGACAGAGCGAGAGCTGCTGGATGGTGTCATAAAGAACTTCGACCTC 1136
Qy 345 ArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeu 364
Db 1137 CGCCCGGGCGTCAATTCAGGGATTGGACTTGAAGAAG-----CCCATCTACCCAG 1187
Qy 365 LysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGluValVal 384
Db 1188 AAGACAGCATGCTACGGCCATTTCGGAAGAAGC-----GAGTTCCCATGGGAGGTTCCC 1241
Qy 385 LysProLeu 387
Db 1242 AGGAAGCTT 1250

RESULT 14
US-09-949-016-68
; Sequence 68, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 3228
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-68

Alignment Scores:
Pred. No.: 1,32e-142 Length: 3228
Score: 1274.50 Matches: 241
Percent Similarity: 78.85% Conservative: 61
Best Local Similarity: 62.92% Mismatches: 74
Query Match: 61.19% Indels: 7
DB: 4 Gaps: 3

US-10-734-698A-39 (1-392) x US-09-949-016-68 (1-3228)

Qy 5 PheLeuPheThrSerGluSerValAsnGluGlyHisProAspLysLeuCysAspGlnIle 24
Db 123 TTCATGTTTCACATCGGAGTCTGTGGAGAGGGACACCCCGGATAAGATCTGTGACCCAGATC 182
Qy 25 SerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSerLysValAlaCysGlu 44
Db 183 AGTGATGCAGTGTGTGATGCCCATCTCAAGCAAGACCCCAATGCCAAGGTGGCTGTGTAG 242
Qy 45 ThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThrThrLysAlaAsnVal 64
Db 243 ACAGTGTGCAAGACCGGCGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 302
Qy 65 AspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPheValSerAsnAspVal 84
Db 303 GACTACCACGGGTGTGTGGGACACCATCAAGCACATCGGTACGATGACTCAGCCCAAG 362
Qy 85 GlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGlnGlnSerProAspIle 104
Db 363 GGCTTTGACTTCAAGACTTGCAACGCTGCTGGTGTGGCTTTGGAGCAGCAATCCCCAGATATT 422

Qy 105 AlaGlnGlyValHisGlyHisLeuThrLysArgProGluGluIleGlyAlaGlyAspGln 124
Db 423 GCCCAGTCCGTC-----CATCTGCACAGAAATAGGAGGATGTGGGGCGAGAGATCAG 476
Qy 125 GlyHisMetPheGlyTyrAlaThrAspGluThrProGluLeuMetProLeuSerHisVal 144
Db 477 GGTTTGATGTTTCGGCTATGCTACCGACGAGACAGAGGAGTGCATGCCCTCACCACATCATC 536
Qy 145 LeuAlaThrLysLeuGlyAlaArgLeuThrGluValArgLysAsnGlyThrCysProTrp 164
Db 537 CTTCGTCTCAAGACTCAACGCCCGGATGGCAGACCTCAGCGCTCCGGCTCTCCCTCCCTGG 596
Qy 165 LeuArgProAspGlyLysThrGlnValThrValGluTyrTyrAsnAspAsnGlyAlaMet 184
Db 597 CTGGGCTGACTCTAAGACTCAGGTGACGTTTCAGTACATGCAGACACATGGCCGACGTC 656
Qy 185 ValProValArgValHisThrValLeuIleSerThrGlnHisAspGluThrValThrAsn 204
Db 657 ATCCCTGTGGCATCCACCATCTCTCTGTGCAGACACAAACGAAGACATCAGCGTG 716
Qy 205 AspGluIleAlaAlaAspLeuLysGluHisValIleLysProValIleProGluLysTyr 224
Db 717 GAGGAGATGCGCAGCGGCCCTCGAAGGAGCAAGTCTATCAGGGCGGTGGTCCCGGCCAAGTAC 776
Qy 225 LeuAspGluLysThrIlePheHisLeuAsnProSerGlyArgPheValIleGlyPro 244
Db 777 CTGGACGAAGACACCGTCTACCATCTGCAGCCAGCTGGCGGTGTGTGTGTGTGTGTGTGTGT 836
Qy 245 HisGlyAspAlaGlyLeuThrGlyArgLysIleIleAspThrTyrGlyLysTrpGly 264
Db 837 CAGGGGATGCGGGTGTCTACTGGCGTAAGATTATTGTGGACACCATATGGCGGCTGGGG 896
Qy 265 AlaHisGlyGlyAlaPheSerGlyLysAspProThrLysValAspArgSerGlyAla 284
Db 897 GCTCATGTTGGTGGCGCTTCTCTGGGAAGAGACTACACCAAGGTAGACCGCTCAGCTGCA 956
Qy 285 TyrIleValArgGlnAlaAlaLysSerIleValAlaSerGlyLeuAlaArgArgCysIle 304
Db 957 TATGCTGCCCGCTGGTGGCCCAAGTCTCTGTGTGAAGCAGAGGCTCTGCGGAGAGTGCTT 1016
Qy 305 ValGlnValSerTyrAlaIleGlyValProGluProLeuSerValPheValAspThrTyr 324
Db 1017 GTCCAGGTTTCCTATGCTATGTTGGCCGAGCGCTGTCCATTTCCATCTTCCACCTAC 1076
Qy 325 GlyThrGlyLysIleHisAspLysGluIleLeuAsnIleValLysGluAsnPheAspPhe 344
Db 1077 GGAACCTCTCAGAAGACAGAGCGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1136
Qy 345 ArgProGlyMetIleSerIleAsnLeuAspLeuLysArgGlyGlyAsnAsnArgPheLeu 364
Db 1137 CGCCCGGGCGTCAATTCAGGGATTGGACTTGAAGAAG-----CCCATCTACCCAG 1187
Qy 365 LysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrpGluValVal 384
Db 1188 AAGACAGCATGCTACGGCCATTTCGGAAGAAGC-----GAGTTCCCATGGGAGGTTCCC 1241
Qy 385 LysProLeu 387
Db 1242 AGGAAGCTT 1250

RESULT 15
US-09-107-532A-3167
; Sequence 3167, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham

```

STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATON NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 3167:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1215
SEQUENCE DESCRIPTION: SEQ ID NO: 3167:
US-09-107-532A-3167

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Alignment Scores:
Pred. No.: 1.63e-122 Length: 1215
Score: 1102.00 Matches: 223
Percent Similarity: 72.56% Conservative: 60
Best Local Similarity: 57.18% Mismatches: 93
Query Match: 52.90% Indels: 14
DB: 4 Gaps: 5

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US-10-734-698A-39 (1-392) x US-09-107-532A-3167 (1-1215)

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QY 1 MetAlaGluThrPheLeuPheThrSerGluSerValAsnGluGlyHisProAsp---Lys 19
DB 19 ATGGTAGAAGACACTTATTACATCAGATCTGTTCTGAAAGACATCCACGTATATAA 78
QY 20 LeuCysAspGlnIleSerAspAlaValLeuAspAlaCysLeuGluGlnAspProAspSer 39
DB 79 ATTGCTGACCAAAATCAGTGATGCAATCTTGATGCAATTTTAAACAAGATCCACAGCA 138
QY 40 LysValAlaCysGluThrCysThrLysThrAsnLeuValMetValPheGlyGluIleThr 59
DB 139 CGAGTAGCGGTGAAACGCTCTGTAACAACTTGTGTTTATTAGTATTGGAGAAATATCT 198
QY 60 ThrLysAlaAsnValAspTyrGluLysIleValArgAspThrCysArgAsnIleGlyPhe 79
DB 199 ACAGCGCATATGTAGATATTCAAAAGCTGACGGGAACAATAAAGAAATTTGTTAT 258
QY 80 ValSerAsnAspValGlyLeuAspAlaAspAsnCysLysValLeuValAsnIleGluGln 99
DB 259 ACAGGTGCAAAATTCGGATTGATGGAGATACAGCAGCTGTATTGGTTGGATTGATGAA 318
QY 100 GlnSerProAspIleAlaGlnGlyValHisGlyHisLeuThrLysArgProGlu----- 117
DB 319 CAATCTCCTGATATTGCTCAAGGAGTTGATGAAGCACTTGAGATCCGGATGAAGATAAA 378

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QY 118 -----GluIleGlyAlaGlyAspGlnGlyHisMetPheGlyTyrAlaThr 132
DB 379 AAAGACGTATTAGATCAGATGGTGTGTCGACCAAGGTTTAAATGTTTGGTTCGTGTA 438
QY 133 AspGluThrProGluLeuMetProLeuSerHisValLeuAlaThrLysLeuGlyAlaArg 152
DB 439 GATGAACACACAGAAATTGATGCTTTTACCAATCGCTTTCAGTCATCGTGGTACGACGC 498
QY 153 LeuThrGluValArgLysAsnGlyThrCysProTyrLeuArgProAspGlyLysThrGln 172
DB 499 TTGGCAGATTTCGTTAATCAATTAAGTATTACGTCACGATCCAGATCAAAATCTCAA 558
QY 173 ValThrValGluTyrTyrAsnAspAsnGlyAlaMetValProValArgValHisThrVal 192
DB 559 GTAACGGTTGAA---TATGATGATCAAGACAA-----CCGGAACCGCTAGATACAATC 609
QY 193 LeuIleSerThrGlnHisAspGluThrValThrAsnAspGluIleAlaAlaAspLeuLys 212
DB 610 GTTATTTCAACACAGCATGATGATGAGTAGATAATGAACAATTCGTCATGATGTCATC 669
QY 213 GluHisValIleLysProValIleProGluLysTyrLeuAspGluLysThrIlePheHis 232
DB 670 GAAAAGTAGTGAAGAGTTATTCAGCTGAATATTATAGATGATCAACAGAAATATTAT 729
QY 233 LeuAsnProSerGlyArgPheValIleGlyGlyProHisGlyAspAlaGlyLeuThrGly 252
DB 730 ATCAATCCGACTGGCGGATTTCATTTGCTGCTCAAGGGGATCCCGGATTAACAGGA 789
QY 253 ArgLysIleIleAspThrTyrGlyGlyTyrGlyAlaHisGlyGlyGlyAlaPheSer 272
DB 790 AGAAAAATCATTTGATACGTATGCGGTTATGCTGCTGATGGTGGCGGTGCTTTTCT 849
QY 273 GlyLysAspProThrLysValAspArgSerGlyAlaTyrIleValArgGlnAlaLys 292
DB 850 GGTAAAGATGCGCAAAAGTTGACCGTTCTGCCAGCTATGCTGCAGTTATATTGCTAAA 909
QY 293 SerIleValAlaSerGlyLeuAlaArgCysIleValGlnValSerTyrAlaIleGly 312
DB 910 AACATTGTTGCAGCAGGGCTTCTCGCAAGCAGAAAGTACAGCTAGCTATATGCGATTGCT 969
QY 313 ValProGluProLeuSerValPheValAspThrTyrGlyThrGlyLysIleHisAspLys 332
DB 970 GTTGCTCAACCTGTTTCGATCTCAATCAATACTTTTCGGTACTTGGAAACGGTTCGGAAGAA 1029
QY 333 GluIleLeuAsnIleValLysGluAsnPheAspPheArgProGlyMetIleSerIleAsn 352
DB 1030 GAACGTGTTGCTGAGTGAGAGAAAACCTTCGATCTTCGGCCAGCAGGATCATCGAGATG 1089
QY 353 LeuAspLeuLysArgGlyGlyAsnAsnArgPheLeuLysThrAlaAlaTyrGlyHisPhe 372
DB 1090 CTTGATTTGCGTCGT-----CCGATTTACAAACAACAGCTGCTTACGTCATTTT 1140
QY 373 GlyArgGluAspProAspPheThrTrpGlu 382
DB 1141 GGTGCTACAGATGTAGATTTCCTTGGGAA 1170

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Search completed: September 12, 2005, 21:15:32
Job time : 270 secs

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